



1/47

SEQUENCE LISTING

<110> Anderson, Marie  
Fisher, Stewart  
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Lundquist, Rolf T.  
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<120> CRYSTAL STRUCTURE OF GLUTAMATE RACEMASE  
(MURI)

<130> ASZD-P01-007

<140> US 10/729,571

<141> 2003-12-05

<150> US 60/435,167

<151> 2002-12-20

<150> US 60/435,272

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aaa	agc	ctt	tta	aaa	gcg	cga	ttg	ttt	gat	gaa	atc	atc	tac	tat	ggc	96
Lys	Ser	Leu	Leu	Lys	Ala	Arg	Leu	Phe	Asp	Glu	Ile	Ile	Tyr	Tyr	Gly	
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gat	agc	gct	aga	gtg	cct	tat	ggc	act	aaa	gac	ccc	acc	acg	atc	aag	144
Asp	Ser	Ala	Arg	Val	Pro	Tyr	Gly	Thr	Lys	Asp	Pro	Thr	Thr	Ile	Lys	
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caa	ttt	ggc	tta	gag	gct	ttg	gat	ttt	ttc	aaa	ccg	cat	gag	att	gaa	192
Gln	Phe	Gly	Leu	Glu	Ala	Leu	Asp	Phe	Phe	Lys	Pro	His	Glu	Ile	Glu	
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Leu	Leu	Ile	Val	Ala	Cys	Asn	Thr	Ala	Ser	Ala	Leu	Ala	Leu	Glu	Glu		
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Ile	Leu	Ala	Ile	Lys	Arg	Gln	Val	Glu	Asp	Lys	Asn	Ala	Pro	Ile	Leu		
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Val	Leu	Gly	Thr	Lys	Ala	Thr	Ile	Gln	Ser	Asn	Ala	Tyr	Asp	Asn	Ala		
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Phe	Val	Pro	Leu	Ile	Glu	Glu	Ser	Ile	Leu	Glu	Gly	Glu	Leu	Leu	Glu		
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Thr	Cys	Met	His	Tyr	Tyr	Phe	Thr	Pro	Leu	Glu	Ile	Leu	Pro	Glu	Val		
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Ile	Ile	Leu	Gly	Cys	Thr	His	Phe	Pro	Leu	Ile	Ala	Gln	Lys	Ile	Glu		
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ggc	tat	ttc	atg	ggg	cat	ttt	gcc	ctt	cca	acg	ccc	ccc	cta	ctc	atc	624	
Gly	Tyr	Phe	Met	Gly	His	Phe	Ala	Leu	Pro	Thr	Pro	Pro	Leu	Leu	Ile		
		195					200					205					
cat	tcg	ggc	gat	gct	att	gta	gaa	tat	ttg	caa	caa	aaa	tac	gcc	ctt	672	
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		210				215					220						
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Lys	Asn	Asn	Ala	Cys	Thr	Phe	Pro	Lys	Val	Glu	Phe	His	Ala	Ser	Gly		
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gat	gtg	atc	tgg	cta	gaa	aga	caa	gct	aaa	gaa	tgg	ctc	aaa	ttg	taa	768	
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Lys	Ser	Leu	Leu	Lys	Ala	Arg	Leu	Phe	Asp	Glu	Ile	Ile	Tyr	Tyr	Gly		
			20					25					30				

Asp	Ser	Ala	Arg	Val	Pro	Tyr	Gly	Thr	Lys	Asp	Pro	Thr	Thr	Ile	Lys
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Gln	Phe	Gly	Leu	Glu	Ala	Leu	Asp	Phe	Phe	Lys	Pro	His	Glu	Ile	Glu
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Leu	Leu	Ile	Val	Ala	Cys	Asn	Thr	Ala	Ser	Ala	Leu	Ala	Leu	Glu	Glu
65					70					75					80
Met	Gln	Lys	Tyr	Ser	Lys	Ile	Pro	Ile	Val	Gly	Val	Ile	Glu	Pro	Ser
				85					90					95	
Ile	Leu	Ala	Ile	Lys	Arg	Gln	Val	Glu	Asp	Lys	Asn	Ala	Pro	Ile	Leu
			100					105					110		
Val	Leu	Gly	Thr	Lys	Ala	Thr	Ile	Gln	Ser	Asn	Ala	Tyr	Asp	Asn	Ala
		115					120					125			
Leu	Lys	Gln	Gln	Gly	Tyr	Leu	Asn	Ile	Ser	His	Leu	Ala	Thr	Ser	Leu
	130					135					140				
Phe	Val	Pro	Leu	Ile	Glu	Glu	Ser	Ile	Leu	Glu	Gly	Glu	Leu	Leu	Glu
145					150					155					160
Thr	Cys	Met	His	Tyr	Tyr	Phe	Thr	Pro	Leu	Glu	Ile	Leu	Pro	Glu	Val
				165					170					175	
Ile	Ile	Leu	Gly	Cys	Thr	His	Phe	Pro	Leu	Ile	Ala	Gln	Lys	Ile	Glu
			180					185					190		
Gly	Tyr	Phe	Met	Gly	His	Phe	Ala	Leu	Pro	Thr	Pro	Pro	Leu	Leu	Ile
		195					200					205			
His	Ser	Gly	Asp	Ala	Ile	Val	Glu	Tyr	Leu	Gln	Gln	Lys	Tyr	Ala	Leu
	210					215					220				
Lys	Asn	Asn	Ala	Cys	Thr	Phe	Pro	Lys	Val	Glu	Phe	His	Ala	Ser	Gly
225					230					235					240
Asp	Val	Ile	Trp	Leu	Glu	Arg	Gln	Ala	Lys	Glu	Trp	Leu	Lys	Leu	
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aaa	agc	ctt	tta	aaa	gcg	caa	ttg	ttt	gat	gaa	atc	atc	tat	tat	ggc	96
Lys	Ser	Leu	Leu	Lys	Ala	Gln	Leu	Phe	Asp	Glu	Ile	Ile	Tyr	Tyr	Gly	
20				25				30								
gat	agc	gct	aga	gtg	cct	tat	ggc	act	aaa	gac	ccc	act	acg	atc	aag	144
Asp	Ser	Ala	Arg	Val	Pro	Tyr	Gly	Thr	Lys	Asp	Pro	Thr	Thr	Ile	Lys	
35				40				45								
caa	ttt	ggc	tta	gag	gct	ttg	gat	ttt	ttc	aaa	cca	cac	cag	att	gaa	192
Gln	Phe	Gly	Leu	Glu	Ala	Leu	Asp	Phe	Phe	Lys	Pro	His	Gln	Ile	Glu	
50				55				60								
tta	ttg	att	gtg	gca	tgc	aac	acc	gca	agc	gct	ctg	gct	tta	gaa	gag	240
Leu	Leu	Ile	Val	Ala	Cys	Asn	Thr	Ala	Ser	Ala	Leu	Ala	Leu	Glu	Glu	
65				70				75				80				

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atg caa aag cat tcc aaa atc cct att gtg ggc gtg att gag cca agc 288
Met Gln Lys His Ser Lys Ile Pro Ile Val Gly Val Ile Glu Pro Ser
                        85                      90                      95

att tta gcg atc aag caa caa gtg aaa gat aaa aac gcc cct att tta 336
Ile Leu Ala Ile Lys Gln Gln Val Lys Asp Lys Asn Ala Pro Ile Leu
                        100                      105                      110

gtg cta ggg aca aaa gcg acg att caa tcc aac gct tat gac aac gcc 384
Val Leu Gly Thr Lys Ala Thr Ile Gln Ser Asn Ala Tyr Asp Asn Ala
                        115                      120                      125

ctg aaa caa caa ggc tat ttg aat gtt tcg cat tta gcc act tct ctt 432
Leu Lys Gln Gln Gly Tyr Leu Asn Val Ser His Leu Ala Thr Ser Leu
                        130                      135                      140

ttt gtg cct ttg att gaa gaa agt att tta gag ggc gaa ttg tta gag 480
Phe Val Pro Leu Ile Glu Glu Ser Ile Leu Glu Gly Glu Leu Leu Glu
                        145                      150                      155                      160

act tgc atg cgt tat tat ttc act ccc tta aag att tta cct gaa gtg 528
Thr Cys Met Arg Tyr Tyr Phe Thr Pro Leu Lys Ile Leu Pro Glu Val
                        165                      170                      175

att att tta ggt tgc acg cat ttt ccc ttg att gct caa aaa att gag 576
Ile Ile Leu Gly Cys Thr His Phe Pro Leu Ile Ala Gln Lys Ile Glu
                        180                      185                      190

ggc tat ttc atg gag cat ttt gcc ctt cca acg ccc ccc cta ctc atc 624
Gly Tyr Phe Met Glu His Phe Ala Leu Pro Thr Pro Pro Leu Leu Ile
                        195                      200                      205

cat tcg ggc gat gct att gta gaa tat ttg cag caa aaa tac gcc ctt 672
His Ser Gly Asp Ala Ile Val Glu Tyr Leu Gln Gln Lys Tyr Ala Leu
                        210                      215                      220

aaa aac aat gca cac gca ttc cct aaa gtg gaa ttt cat gcg agc ggc 720
Lys Asn Asn Ala His Ala Phe Pro Lys Val Glu Phe His Ala Ser Gly
                        225                      230                      235                      240

gat gtg atc tgg cta gaa aga caa gct aaa gaa tgg ctc aaa ttg taa 768
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<212> PRT
<213> H. pylori

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 20      25      30
Asp Ser Ala Arg Val Pro Tyr Gly Thr Lys Asp Pro Thr Thr Ile Lys
 35      40      45

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Gln	Phe	Gly	Leu	Glu	Ala	Leu	Asp	Phe	Phe	Lys	Pro	His	Gln	Ile	Glu
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Leu	Leu	Ile	Val	Ala	Cys	Asn	Thr	Ala	Ser	Ala	Leu	Ala	Leu	Glu	Glu
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Met	Gln	Lys	His	Ser	Lys	Ile	Pro	Ile	Val	Gly	Val	Ile	Glu	Pro	Ser
				85					90					95	
Ile	Leu	Ala	Ile	Lys	Gln	Gln	Val	Lys	Asp	Lys	Asn	Ala	Pro	Ile	Leu
			100					105					110		
Val	Leu	Gly	Thr	Lys	Ala	Thr	Ile	Gln	Ser	Asn	Ala	Tyr	Asp	Asn	Ala
		115					120					125			
Leu	Lys	Gln	Gln	Gly	Tyr	Leu	Asn	Val	Ser	His	Leu	Ala	Thr	Ser	Leu
	130					135					140				
Phe	Val	Pro	Leu	Ile	Glu	Glu	Ser	Ile	Leu	Glu	Gly	Glu	Leu	Leu	Glu
145					150					155					160
Thr	Cys	Met	Arg	Tyr	Tyr	Phe	Thr	Pro	Leu	Lys	Ile	Leu	Pro	Glu	Val
				165					170					175	
Ile	Ile	Leu	Gly	Cys	Thr	His	Phe	Pro	Leu	Ile	Ala	Gln	Lys	Ile	Glu
			180					185					190		
Gly	Tyr	Phe	Met	Glu	His	Phe	Ala	Leu	Pro	Thr	Pro	Pro	Leu	Leu	Ile
	195						200					205			
His	Ser	Gly	Asp	Ala	Ile	Val	Glu	Tyr	Leu	Gln	Gln	Lys	Tyr	Ala	Leu
	210					215					220				
Lys	Asn	Asn	Ala	His	Ala	Phe	Pro	Lys	Val	Glu	Phe	His	Ala	Ser	Gly
225					230					235					240
Asp	Val	Ile	Trp	Leu	Glu	Arg	Gln	Ala	Lys	Glu	Trp	Leu	Lys	Leu	
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 <213> H. pylori

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1				5					10					15		
aaa agc ctt tta aaa gcg caa tta ttt gat gaa atc atc tat tat ggc																96
Lys	Ser	Leu	Leu	Lys	Ala	Gln	Leu	Phe	Asp	Glu	Ile	Ile	Tyr	Tyr	Gly	
			20					25					30			
gat agc gct aga gtg cct tat ggc act aaa gac ccc act acg atc aag																144
Asp	Ser	Ala	Arg	Val	Pro	Tyr	Gly	Thr	Lys	Asp	Pro	Thr	Thr	Ile	Lys	
			35				40					45				
caa ttt ggc tta gag gct ttg gat ttt ttc aaa ccg cac cag att gaa																192
Gln	Phe	Gly	Leu	Glu	Ala	Leu	Asp	Phe	Phe	Lys	Pro	His	Gln	Ile	Glu	
			50				55				60					
tta ttg att gtg gca tgc aac aca gcg agc gct cta gct tta gaa gag																240
Leu	Leu	Ile	Val	Ala	Cys	Asn	Thr	Ala	Ser	Ala	Leu	Ala	Leu	Glu	Glu	
					70					75					80	
atg caa aag cat tcc aaa atc cct att gtg ggc gtg att gag cca agc																288

Met	Gln	Lys	His	Ser	Lys	Ile	Pro	Ile	Val	Gly	Val	Ile	Glu	Pro	Ser		
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Ile	Leu	Ala	Ile	Lys	Arg	Gln	Val	Lys	Asp	Lys	Asn	Ala	Pro	Ile	Leu		
			100					105					110				
gtg	cta	ggg	aca	aaa	gcg	acg	atc	caa	tcc	aac	gct	tat	gac	aat	gcc	384	
Val	Leu	Gly	Thr	Lys	Ala	Thr	Ile	Gln	Ser	Asn	Ala	Tyr	Asp	Asn	Ala		
		115					120					125					
ctg	aaa	caa	caa	ggc	tat	ttg	aat	gtt	tgc	cat	tta	gcc	act	tct	ctt	432	
Leu	Lys	Gln	Gln	Gly	Tyr	Leu	Asn	Val	Ser	His	Leu	Ala	Thr	Ser	Leu		
	130					135					140						
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Phe	Val	Pro	Leu	Ile	Glu	Glu	Ser	Ile	Leu	Glu	Gly	Glu	Leu	Leu	Glu		
145					150				155						160		
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Thr	Cys	Met	Arg	Tyr	Tyr	Phe	Thr	Pro	Leu	Lys	Ile	Leu	Pro	Glu	Val		
			165					170					175				
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Ile	Ile	Leu	Gly	Cys	Thr	His	Phe	Pro	Leu	Ile	Ala	Gln	Lys	Ile	Glu		
		180					185						190				
ggc	tat	ttt	atg	gag	cat	ttt	gcc	ctt	tca	aca	ccc	ccc	cta	ctc	atc	624	
Gly	Tyr	Phe	Met	Glu	His	Phe	Ala	Leu	Ser	Thr	Pro	Pro	Leu	Leu	Ile		
		195					200					205					
cat	tgc	ggc	gat	gct	att	gta	gga	tat	ttg	cag	caa	aaa	tac	gcc	ctt	672	
His	Ser	Gly	Asp	Ala	Ile	Val	Gly	Tyr	Leu	Gln	Gln	Lys	Tyr	Ala	Leu		
	210				215						220						
aaa	aaa	aat	gca	cac	gca	ttc	cct	aaa	gtg	gaa	ttt	cat	gcg	agc	ggc	720	
Lys	Lys	Asn	Ala	His	Ala	Phe	Pro	Lys	Val	Glu	Phe	His	Ala	Ser	Gly		
225					230				235						240		
gat	gtg	atc	tgg	cta	gaa	aaa	caa	gct	aaa	gaa	tgg	ctc	aaa	ttg	taa	768	
Asp	Val	Ile	Trp	Leu	Glu	Lys	Gln	Ala	Lys	Glu	Trp	Leu	Lys	Leu	*		
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 Asp Ser Ala Arg Val Pro Tyr Gly Thr Lys Asp Pro Thr Thr Ile Lys  
 35 40 45  
 Gln Phe Gly Leu Glu Ala Leu Asp Phe Phe Lys Pro His Gln Ile Glu  
 50 55 60

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Leu Leu Ile Val Ala Cys Asn Thr Ala Ser Ala Leu Ala Leu Glu Glu
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Met Gln Lys His Ser Lys Ile Pro Ile Val Gly Val Ile Glu Pro Ser
      85      90      95
Ile Leu Ala Ile Lys Arg Gln Val Lys Asp Lys Asn Ala Pro Ile Leu
      100     105     110
Val Leu Gly Thr Lys Ala Thr Ile Gln Ser Asn Ala Tyr Asp Asn Ala
      115     120     125
Leu Lys Gln Gln Gly Tyr Leu Asn Val Ser His Leu Ala Thr Ser Leu
      130     135     140
Phe Val Pro Leu Ile Glu Glu Ser Ile Leu Glu Gly Glu Leu Leu Glu
145     150     155     160
Thr Cys Met Arg Tyr Phe Thr Pro Leu Lys Ile Leu Pro Glu Val
      165     170     175
Ile Ile Leu Gly Cys Thr His Phe Pro Leu Ile Ala Gln Lys Ile Glu
      180     185     190
Gly Tyr Phe Met Glu His Phe Ala Leu Ser Thr Pro Pro Leu Leu Ile
      195     200     205
His Ser Gly Asp Ala Ile Val Gly Tyr Leu Gln Gln Lys Tyr Ala Leu
      210     215     220
Lys Lys Asn Ala His Ala Phe Pro Lys Val Glu Phe His Ala Ser Gly
225     230     235     240
Asp Val Ile Trp Leu Glu Lys Gln Ala Lys Glu Trp Leu Lys Leu
      245     250     255

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<210> 7  
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<220>  
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 <222> (1)...(747)

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aaa agc ctt tta aaa gcg caa ttg ttt gat gaa atc atc tat tat ggc 96
Lys Ser Leu Leu Lys Ala Gln Leu Phe Asp Glu Ile Ile Tyr Tyr Gly
      20      25      30

gat agc gct aga gtg cct tat ggc act aaa gac ccc acc acg atc aag 144
Asp Ser Ala Arg Val Pro Tyr Gly Thr Lys Asp Pro Thr Thr Ile Lys
      35      40      45

caa ttt ggc tta gag gct ttg gat ttt ttc aaa ccg cac cag att aaa 192
Gln Phe Gly Leu Glu Ala Leu Asp Phe Phe Lys Pro His Gln Ile Lys
      50      55      60

tta ttg att gtg gca tgc aac aca gcg agc gct cta gct tta gaa gag 240
Leu Leu Ile Val Ala Cys Asn Thr Ala Ser Ala Leu Ala Leu Glu Glu
65      70      75      80

atg caa aag cat tcc aaa atc cct att gtg ggc gtg att gag cca agc 288
Met Gln Lys His Ser Lys Ile Pro Ile Val Gly Val Ile Glu Pro Ser
      85      90      95

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att tta gcg atc aag caa caa gta aaa gat aaa aac gcc cct att tta 336
Ile Leu Ala Ile Lys Gln Gln Val Lys Asp Lys Asn Ala Pro Ile Leu
100 105 110

gtg cta ggg aca aaa gcg acg atc caa tcc aac gct tat gac aac gcc 384
Val Leu Gly Thr Lys Ala Thr Ile Gln Ser Asn Ala Tyr Asp Asn Ala
115 120 125

ctg aaa caa caa ggc tat ttg aat gtt tcg cat tta gcc act tct ctt 432
Leu Lys Gln Gln Gly Tyr Leu Asn Val Ser His Leu Ala Thr Ser Leu
130 135 140

ttt gtg cct ttg att gaa gaa agt att tta ggg ggc gaa ttg tta gaa 480
Phe Val Pro Leu Ile Glu Glu Ser Ile Leu Gly Gly Glu Leu Leu Glu
145 150 155 160

act tgc atg cgt tat tat ttc act ccc tta aag att tta cct gaa gtg 528
Thr Cys Met Arg Tyr Tyr Phe Thr Pro Leu Lys Ile Leu Pro Glu Val
165 170 175

att att tta ggt tgc acg cat ttt ccc ttg atc gct caa aaa att gag 576
Ile Ile Leu Gly Cys Thr His Phe Pro Leu Ile Ala Gln Lys Ile Glu
180 185 190

ggc tat ttt atg gag cat ttt gcc ctt tca acg ccc ccc cta ctc atc 624
Gly Tyr Phe Met Glu His Phe Ala Leu Ser Thr Pro Pro Leu Leu Ile
195 200 205

cat tcg ggc gat gct att gtg gaa tat ttg cag caa aaa tac gcc ctt 672
His Ser Gly Asp Ala Ile Val Glu Tyr Leu Gln Gln Lys Tyr Ala Leu
210 215 220

aag aaa aat gca cac gca ttc cct aaa gtg gaa ttt cat gcg agc ggc 720
Lys Lys Asn Ala His Ala Phe Pro Lys Val Glu Phe His Ala Ser Gly
225 230 235 240

gat gtg atc tgg cta gaa aaa cag gct aa 749
Asp Val Ile Trp Leu Glu Lys Gln Ala
245

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&lt;210&gt; 8

&lt;211&gt; 249

&lt;212&gt; PRT

&lt;213&gt; H. pylori

&lt;400&gt; 8

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1 5 10 15
Lys Ser Leu Leu Lys Ala Gln Leu Phe Asp Glu Ile Ile Tyr Tyr Gly
20 25 30
Asp Ser Ala Arg Val Pro Tyr Gly Thr Lys Asp Pro Thr Thr Ile Lys
35 40 45
Gln Phe Gly Leu Glu Ala Leu Asp Phe Phe Lys Pro His Gln Ile Lys
50 55 60
Leu Leu Ile Val Ala Cys Asn Thr Ala Ser Ala Leu Ala Leu Glu Glu
65 70 75 80

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Met	Gln	Lys	His	Ser	Lys	Ile	Pro	Ile	Val	Gly	Val	Ile	Glu	Pro	Ser	
				85					90					95		
Ile	Leu	Ala	Ile	Lys	Gln	Gln	Val	Lys	Asp	Lys	Asn	Ala	Pro	Ile	Leu	
			100					105					110			
Val	Leu	Gly	Thr	Lys	Ala	Thr	Ile	Gln	Ser	Asn	Ala	Tyr	Asp	Asn	Ala	
		115					120					125				
Leu	Lys	Gln	Gln	Gly	Tyr	Leu	Asn	Val	Ser	His	Leu	Ala	Thr	Ser	Leu	
	130					135					140					
Phe	Val	Pro	Leu	Ile	Glu	Glu	Ser	Ile	Leu	Gly	Gly	Glu	Leu	Leu	Glu	
145					150					155					160	
Thr	Cys	Met	Arg	Tyr	Tyr	Phe	Thr	Pro	Leu	Lys	Ile	Leu	Pro	Glu	Val	
			165					170						175		
Ile	Ile	Leu	Gly	Cys	Thr	His	Phe	Pro	Leu	Ile	Ala	Gln	Lys	Ile	Glu	
		180						185					190			
Gly	Tyr	Phe	Met	Glu	His	Phe	Ala	Leu	Ser	Thr	Pro	Pro	Leu	Leu	Ile	
	195						200					205				
His	Ser	Gly	Asp	Ala	Ile	Val	Glu	Tyr	Leu	Gln	Gln	Lys	Tyr	Ala	Leu	
	210					215					220					
Lys	Lys	Asn	Ala	His	Ala	Phe	Pro	Lys	Val	Glu	Phe	His	Ala	Ser	Gly	
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Asp	Val	Ile	Trp	Leu	Glu	Lys	Gln	Ala								
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 <213> H. pylori

<220>  
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1 5 10 15	
aaa agc ctt tta aaa gcg caa cta ttt gat gaa atc atc tat tat ggc	96
Lys Ser Leu Leu Lys Ala Gln Leu Phe Asp Glu Ile Ile Tyr Tyr Gly	
20 25 30	
gat agt gct aga gtg cct tat ggc act aaa gac ccc acc acg atc aag	144
Asp Ser Ala Arg Val Pro Tyr Gly Thr Lys Asp Pro Thr Thr Ile Lys	
35 40 45	
caa ttt ggc tta gag gct ttg gat ttt ttc aaa ccg cac cag att gga	192
Gln Phe Gly Leu Glu Ala Leu Asp Phe Phe Lys Pro His Gln Ile Gly	
50 55 60	
tta ttg att gtg gca tgc aac aca gcg agc gct cta gct tta gaa gag	240
Leu Leu Ile Val Ala Cys Asn Thr Ala Ser Ala Leu Ala Leu Glu Glu	
65 70 75 80	
atg caa aag cat tcc aaa atc cct att gtg ggc gtg att gaa cca agc	288
Met Gln Lys His Ser Lys Ile Pro Ile Val Gly Val Ile Glu Pro Ser	
85 90 95	
att tta gcg atc aag caa caa gta aaa gat aaa aac gcc tct att ttg	336

Ile	Leu	Ala	Ile	Lys	Gln	Gln	Val	Lys	Asp	Lys	Asn	Ala	Ser	Ile	Leu	
			100					105					110			
gtg	cta	ggg	aca	aaa	gcg	acg	atc	caa	tcc	aac	gct	tat	gac	aac	gcc	384
Val	Leu	Gly	Thr	Lys	Ala	Thr	Ile	Gln	Ser	Asn	Ala	Tyr	Asp	Asn	Ala	
		115					120					125				
ctg	aaa	caa	caa	ggc	tat	ttg	aat	gtt	tcg	cat	tta	gcc	act	tct	ctt	432
Leu	Lys	Gln	Gln	Gly	Tyr	Leu	Asn	Val	Ser	His	Leu	Ala	Thr	Ser	Leu	
	130					135					140					
ttt	gtg	cct	ttg	att	gaa	gaa	agt	att	tta	gag	ggc	gaa	ttg	cta	gaa	480
Phe	Val	Pro	Leu	Ile	Glu	Glu	Ser	Ile	Leu	Glu	Gly	Glu	Leu	Leu	Glu	
145					150					155					160	
act	tgc	atg	cgt	tat	tat	ttc	act	ccg	tta	gag	atc	ttg	cct	gaa	gtg	528
Thr	Cys	Met	Arg	Tyr	Tyr	Phe	Thr	Pro	Leu	Glu	Ile	Leu	Pro	Glu	Val	
			165					170						175		
gtt	att	tta	ggc	tgc	acg	cat	ttt	ccc	tta	atc	gct	caa	aaa	att	gag	576
Val	Ile	Leu	Gly	Cys	Thr	His	Phe	Pro	Leu	Ile	Ala	Gln	Lys	Ile	Glu	
		180					185						190			
ggc	tat	ttt	atg	gag	cat	ttt	gcc	ctt	tca	acg	ccc	ccc	cta	ctc	atc	624
Gly	Tyr	Phe	Met	Glu	His	Phe	Ala	Leu	Ser	Thr	Pro	Pro	Leu	Leu	Ile	
		195					200					205				
cat	tcg	ggc	gat	gct	att	gtg	gaa	tat	ttg	cag	caa	aaa	tac	gcc	ctt	672
His	Ser	Gly	Asp	Ala	Ile	Val	Glu	Tyr	Leu	Gln	Gln	Lys	Tyr	Ala	Leu	
	210				215					220						
aaa	aaa	aat	gca	cac	gca	ttc	cct	aaa	gtg	gaa	ttt	cat	gcg	agt	ggc	720
Lys	Lys	Asn	Ala	His	Ala	Phe	Pro	Lys	Val	Glu	Phe	His	Ala	Ser	Gly	
225					230					235					240	
gat	gtg	atc	tgg	cta	gaa	aaa	cag	gct	aaa	gaa	tgg	ctc	aaa	ttg	taa	768
Asp	Val	Ile	Trp	Leu	Glu	Lys	Gln	Ala	Lys	Glu	Trp	Leu	Lys	Leu	*	
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 <212> PRT  
 <213> H. pylori

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 1 5 10 15  
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 20 25 30  
 Asp Ser Ala Arg Val Pro Tyr Gly Thr Lys Asp Pro Thr Thr Ile Lys  
 35 40 45  
 Gln Phe Gly Leu Glu Ala Leu Asp Phe Phe Lys Pro His Gln Ile Gly  
 50 55 60  
 Leu Leu Ile Val Ala Cys Asn Thr Ala Ser Ala Leu Ala Leu Glu Glu  
 65 70 75 80  
 Met Gln Lys His Ser Lys Ile Pro Ile Val Gly Val Ile Glu Pro Ser  
 85 90 95

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Ile Leu Ala Ile Lys Gln Gln Val Lys Asp Lys Asn Ala Ser Ile Leu
      100      105      110
Val Leu Gly Thr Lys Ala Thr Ile Gln Ser Asn Ala Tyr Asp Asn Ala
      115      120      125
Leu Lys Gln Gln Gly Tyr Leu Asn Val Ser His Leu Ala Thr Ser Leu
      130      135      140
Phe Val Pro Leu Ile Glu Glu Ser Ile Leu Glu Gly Glu Leu Leu Glu
      145      150      155      160
Thr Cys Met Arg Tyr Tyr Phe Thr Pro Leu Glu Ile Leu Pro Glu Val
      165      170      175
Val Ile Leu Gly Cys Thr His Phe Pro Leu Ile Ala Gln Lys Ile Glu
      180      185      190
Gly Tyr Phe Met Glu His Phe Ala Leu Ser Thr Pro Pro Leu Leu Ile
      195      200      205
His Ser Gly Asp Ala Ile Val Glu Tyr Leu Gln Gln Lys Tyr Ala Leu
      210      215      220
Lys Lys Asn Ala His Ala Phe Pro Lys Val Glu Phe His Ala Ser Gly
      225      230      235      240
Asp Val Ile Trp Leu Glu Lys Gln Ala Lys Glu Trp Leu Lys Leu
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 <213> H. pylori

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aaa agc ctt tta aaa gcg caa att ttt gat gaa atc atc tat tat ggc 96
Lys Ser Leu Leu Lys Ala Gln Ile Phe Asp Glu Ile Ile Tyr Tyr Gly
      20          25          30

gat agc gct aga gtg cct tat ggc act aaa gac ccc acc acg atc aag 144
Asp Ser Ala Arg Val Pro Tyr Gly Thr Lys Asp Pro Thr Thr Ile Lys
      35          40          45

caa ttt ggc tta gag gct ttg gat ttt ttc aaa ccg cac cag att aaa 192
Gln Phe Gly Leu Glu Ala Leu Asp Phe Phe Lys Pro His Gln Ile Lys
      50          55          60

tta ttg att gtg gca tgc aac aca gcg agc gct cta gct tta gaa gag 240
Leu Leu Ile Val Ala Cys Asn Thr Ala Ser Ala Leu Ala Leu Glu Glu
      65          70          75          80

atg caa aag cat tcc aaa atc cct att gtg ggc gtg att gag cca agc 288
Met Gln Lys His Ser Lys Ile Pro Ile Val Gly Val Ile Glu Pro Ser
      85          90          95

att tta gcg atc aag caa caa gta aaa gat aaa aac gcc cct att tta 336
Ile Leu Ala Ile Lys Gln Gln Val Lys Asp Lys Asn Ala Pro Ile Leu
      100          105          110

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gtg cta ggg aca aaa gcg acg att caa tct aac gct tat gac aac gcc	384
Val Leu Gly Thr Lys Ala Thr Ile Gln Ser Asn Ala Tyr Asp Asn Ala	
115 120 125	
cta aaa caa caa ggc tat ttg aac att tcg cat tta gcc act tct ctt	432
Leu Lys Gln Gln Gly Tyr Leu Asn Ile Ser His Leu Ala Thr Ser Leu	
130 135 140	
ttt gtg cct ttg att gaa gaa agt att tta gag ggc gaa ttg tta gag	480
Phe Val Pro Leu Ile Glu Glu Ser Ile Leu Glu Gly Glu Leu Leu Glu	
145 150 155 160	
act tgc atg cgt tat tat ttc act ccc tta aag att tta cct gaa gtg	528
Thr Cys Met Arg Tyr Tyr Phe Thr Pro Leu Lys Ile Leu Pro Glu Val	
165 170 175	
atc att tta ggt tgc acg cat ttt ccc ttg atc gct caa aaa att gag	576
Ile Ile Leu Gly Cys Thr His Phe Pro Leu Ile Ala Gln Lys Ile Glu	
180 185 190	
ggc tat ttt atg gag cat ttt gcc ctt cca acc ccc ccc cta ctc atc	624
Gly Tyr Phe Met Glu His Phe Ala Leu Pro Thr Pro Pro Leu Leu Ile	
195 200 205	
cat tcg ggc gat gct att gta gaa tat ttg cag caa aaa tac acc ctt	672
His Ser Gly Asp Ala Ile Val Glu Tyr Leu Gln Gln Lys Tyr Thr Leu	
210 215 220	
aag aaa aat gca cac gca ttc cct aaa gtg gaa ttt cat gcg agt ggc	720
Lys Lys Asn Ala His Ala Phe Pro Lys Val Glu Phe His Ala Ser Gly	
225 230 235 240	
gat gtg gtt tgg cta gaa aaa cag gct aa	749
Asp Val Val Trp Leu Glu Lys Gln Ala	
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20 25 30	
Asp Ser Ala Arg Val Pro Tyr Gly Thr Lys Asp Pro Thr Thr Ile Lys	
35 40 45	
Gln Phe Gly Leu Glu Ala Leu Asp Phe Phe Lys Pro His Gln Ile Lys	
50 55 60	
Leu Leu Ile Val Ala Cys Asn Thr Ala Ser Ala Leu Ala Leu Glu Glu	
65 70 75 80	
Met Gln Lys His Ser Lys Ile Pro Ile Val Gly Val Ile Glu Pro Ser	
85 90 95	
Ile Leu Ala Ile Lys Gln Gln Val Lys Asp Lys Asn Ala Pro Ile Leu	
100 105 110	

Val	Leu	Gly	Thr	Lys	Ala	Thr	Ile	Gln	Ser	Asn	Ala	Tyr	Asp	Asn	Ala
	115						120					125			
Leu	Lys	Gln	Gln	Gly	Tyr	Leu	Asn	Ile	Ser	His	Leu	Ala	Thr	Ser	Leu
	130					135					140				
Phe	Val	Pro	Leu	Ile	Glu	Glu	Ser	Ile	Leu	Glu	Gly	Glu	Leu	Leu	Glu
145					150					155					160
Thr	Cys	Met	Arg	Tyr	Tyr	Phe	Thr	Pro	Leu	Lys	Ile	Leu	Pro	Glu	Val
				165					170					175	
Ile	Ile	Leu	Gly	Cys	Thr	His	Phe	Pro	Leu	Ile	Ala	Gln	Lys	Ile	Glu
			180					185					190		
Gly	Tyr	Phe	Met	Glu	His	Phe	Ala	Leu	Pro	Thr	Pro	Pro	Leu	Leu	Ile
	195						200					205			
His	Ser	Gly	Asp	Ala	Ile	Val	Glu	Tyr	Leu	Gln	Gln	Lys	Tyr	Thr	Leu
	210					215				220					
Lys	Lys	Asn	Ala	His	Ala	Phe	Pro	Lys	Val	Glu	Phe	His	Ala	Ser	Gly
225					230					235					240
Asp	Val	Val	Trp	Leu	Glu	Lys	Gln	Ala							
				245											

<210> 13  
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<220>  
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Met	Lys	Ile	Gly	Val	Phe	Asp	Ser	Gly	Val	Gly	Gly	Phe	Ser	Val	Leu	
1				5					10					15		
aaa agc ctt tta aaa gcg caa att ttt gat gaa atc atc tat tat ggc															96	
Lys	Ser	Leu	Leu	Lys	Ala	Gln	Ile	Phe	Asp	Glu	Ile	Ile	Tyr	Tyr	Gly	
			20					25					30			
gat agt gct aga gtg cct tat ggc act aaa gac ccc acc acg atc aag															144	
Asp	Ser	Ala	Arg	Val	Pro	Tyr	Gly	Thr	Lys	Asp	Pro	Thr	Thr	Ile	Lys	
			35				40					45				
caa ttt ggc tta gag gct ttg gat ttt ttc aaa ccg cac cag att gga															192	
Gln	Phe	Gly	Leu	Glu	Ala	Leu	Asp	Phe	Phe	Lys	Pro	His	Gln	Ile	Gly	
			50			55					60					
tta ttg att gtg gca tgc aac aca gcg agc gct cta gct tta gaa gag															240	
Leu	Leu	Ile	Val	Ala	Cys	Asn	Thr	Ala	Ser	Ala	Leu	Ala	Leu	Glu	Glu	
	65				70				75					80		
atg caa aag cat tcc aaa atc cct att gtg ggc gtg att gag cca agc															288	
Met	Gln	Lys	His	Ser	Lys	Ile	Pro	Ile	Val	Gly	Val	Ile	Glu	Pro	Ser	
			85						90				95			
att tta gcg atc aaa caa caa gtg aaa gat aaa aac gct cct att tta															336	
Ile	Leu	Ala	Ile	Lys	Gln	Gln	Val	Lys	Asp	Lys	Asn	Ala	Pro	Ile	Leu	
			100					105					110			
gtg cta ggg aca aaa gcg acg att caa tct aac gct tac gat aac gcc															384	

Val	Leu	Gly	Thr	Lys	Ala	Thr	Ile	Gln	Ser	Asn	Ala	Tyr	Asp	Asn	Ala		
		115					120					125					
ctg	aaa	caa	caa	ggc	tat	ttg	aat	ggt	tcg	cat	tta	gcc	act	tct	ctt	432	
Leu	Lys	Gln	Gln	Gly	Tyr	Leu	Asn	Val	Ser	His	Leu	Ala	Thr	Ser	Leu		
		130				135					140						
ttt	gtg	cct	ttg	att	gaa	gaa	aat	att	tta	gag	ggc	gaa	ttg	cta	gaa	480	
Phe	Val	Pro	Leu	Ile	Glu	Glu	Asn	Ile	Leu	Glu	Gly	Glu	Leu	Leu	Glu		
					150					155					160		
act	tgc	atg	cgt	tat	tat	ttc	act	ccc	tta	aag	att	tta	cct	gaa	gtg	528	
Thr	Cys	Met	Arg	Tyr	Tyr	Phe	Thr	Pro	Leu	Lys	Ile	Leu	Pro	Glu	Val		
				165					170					175			
atc	att	tta	ggt	tgc	acg	cat	ttt	ccc	ttg	atc	gct	caa	aaa	att	gag	576	
Ile	Ile	Leu	Gly	Cys	Thr	His	Phe	Pro	Leu	Ile	Ala	Gln	Lys	Ile	Glu		
			180					185					190				
ggc	tat	ttt	atg	gag	cat	ttt	gcc	ctt	tta	acg	ccc	ccc	cta	ctc	atc	624	
Gly	Tyr	Phe	Met	Glu	His	Phe	Ala	Leu	Leu	Thr	Pro	Pro	Leu	Leu	Ile		
		195					200					205					
cat	tct	ggc	gat	gct	att	gta	gaa	tat	ttg	caa	caa	aaa	tac	gcc	ctt	672	
His	Ser	Gly	Asp	Ala	Ile	Val	Glu	Tyr	Leu	Gln	Gln	Lys	Tyr	Ala	Leu		
		210				215					220						
aag	aaa	aat	gca	cac	tca	ttc	cct	aaa	gtg	gaa	ttt	cat	gcg	agc	ggc	720	
Lys	Lys	Asn	Ala	His	Ser	Phe	Pro	Lys	Val	Glu	Phe	His	Ala	Ser	Gly		
		225			230				235						240		
gat	gtg	atc	tgg	cta	gaa	aaa	cag	gct	aaa	gaa	tgg	ctc	aaa	ttg	taa	768	
Asp	Val	Ile	Trp	Leu	Glu	Lys	Gln	Ala	Lys	Glu	Trp	Leu	Lys	Leu	*		
				245					250					255			

<210> 14  
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 <212> PRT  
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<400> 14

Met	Lys	Ile	Gly	Val	Phe	Asp	Ser	Gly	Val	Gly	Gly	Phe	Ser	Val	Leu		
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Lys	Ser	Leu	Leu	Lys	Ala	Gln	Ile	Phe	Asp	Glu	Ile	Ile	Tyr	Tyr	Gly		
		20						25					30				
Asp	Ser	Ala	Arg	Val	Pro	Tyr	Gly	Thr	Lys	Asp	Pro	Thr	Thr	Ile	Lys		
		35					40					45					
Gln	Phe	Gly	Leu	Glu	Ala	Leu	Asp	Phe	Phe	Lys	Pro	His	Gln	Ile	Gly		
	50				55						60						
Leu	Leu	Ile	Val	Ala	Cys	Asn	Thr	Ala	Ser	Ala	Leu	Ala	Leu	Glu	Glu		
					70				75					80			
Met	Gln	Lys	His	Ser	Lys	Ile	Pro	Ile	Val	Gly	Val	Ile	Glu	Pro	Ser		
				85					90					95			
Ile	Leu	Ala	Ile	Lys	Gln	Gln	Val	Lys	Asp	Lys	Asn	Ala	Pro	Ile	Leu		
		100					105						110				
Val	Leu	Gly	Thr	Lys	Ala	Thr	Ile	Gln	Ser	Asn	Ala	Tyr	Asp	Asn	Ala		
		115					120						125				

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Leu Lys Gln Gln Gly Tyr Leu Asn Val Ser His Leu Ala Thr Ser Leu
  130          135          140
Phe Val Pro Leu Ile Glu Glu Asn Ile Leu Glu Gly Glu Leu Leu Glu
145          150          155          160
Thr Cys Met Arg Tyr Phe Thr Pro Leu Lys Ile Leu Pro Glu Val
          165          170          175
Ile Ile Leu Gly Cys Thr His Phe Pro Leu Ile Ala Gln Lys Ile Glu
          180          185          190
Gly Tyr Phe Met Glu His Phe Ala Leu Leu Thr Pro Pro Leu Leu Ile
          195          200          205
His Ser Gly Asp Ala Ile Val Glu Tyr Leu Gln Gln Lys Tyr Ala Leu
          210          215          220
Lys Lys Asn Ala His Ser Phe Pro Lys Val Glu Phe His Ala Ser Gly
225          230          235          240
Asp Val Ile Trp Leu Glu Lys Gln Ala Lys Glu Trp Leu Lys Leu
          245          250          255

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<210> 15  
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<220>  
 <221> CDS  
 <222> (1)...(768)

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Met Lys Ile Gly Val Phe Asp Ser Gly Val Gly Gly Phe Ser Val Leu
  1          5          10          15

aaa agc ctt tta aaa gcg caa att ttt gat gaa atc atc tat tat ggc 96
Lys Ser Leu Leu Lys Ala Gln Ile Phe Asp Glu Ile Ile Tyr Tyr Gly
          20          25          30

gat agc gct aga gtg cct tat ggc act aaa gac ccc acc acg atc aag 144
Asp Ser Ala Arg Val Pro Tyr Gly Thr Lys Asp Pro Thr Thr Ile Lys
          35          40          45

caa ttt ggc tta gag gct ttg gat ttt ttc aaa ccg cac cag att gaa 192
Gln Phe Gly Leu Glu Ala Leu Asp Phe Phe Lys Pro His Gln Ile Glu
          50          55          60

tta ttg att gtg gca tgc aac aca gcg agc gct cta gct tta gaa gag 240
Leu Leu Ile Val Ala Cys Asn Thr Ala Ser Ala Leu Ala Leu Glu Glu
          65          70          75          80

atg caa aag cat tcc aaa atc cct att gtg ggc gtg att gaa cca agc 288
Met Gln Lys His Ser Lys Ile Pro Ile Val Gly Val Ile Glu Pro Ser
          85          90          95

att tta gcg atc aaa caa caa gtg aaa gat aaa aac gct cct att tta 336
Ile Leu Ala Ile Lys Gln Gln Val Lys Asp Lys Asn Ala Pro Ile Leu
          100          105          110

gtg cta ggg aca aaa gcg acg att caa tct aac gct tac gac aac gcc 384
Val Leu Gly Thr Lys Ala Thr Ile Gln Ser Asn Ala Tyr Asp Asn Ala
          115          120          125

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ctg aaa caa caa ggc tat ttg aat gtt tcg cat tta gcc act tct ctt 432
Leu Lys Gln Gln Gly Tyr Leu Asn Val Ser His Leu Ala Thr Ser Leu
130 135 140

ttt gtg cct ttg att gaa gaa agt att tta gag ggc gaa ttg cta gaa 480
Phe Val Pro Leu Ile Glu Glu Ser Ile Leu Glu Gly Glu Leu Leu Glu
145 150 155 160

act tgc atg cgt tat tat ttc act ccc tta aag att tta ccc aaa gta 528
Thr Cys Met Arg Tyr Tyr Phe Thr Pro Leu Lys Ile Leu Pro Lys Val
165 170 175

atc att tta ggt tgc acg cat ttt ccc ttg atc gct cac caa att aag 576
Ile Ile Leu Gly Cys Thr His Phe Pro Leu Ile Ala His Gln Ile Lys
180 185 190

ggc tat ttt atg ggg cat ttt gcc ctt tca acg ccc ccc cta ctc atc 624
Gly Tyr Phe Met Gly His Phe Ala Leu Ser Thr Pro Pro Leu Leu Ile
195 200 205

cat tcg ggc gat gct att gtg gga tat ttg caa caa aaa tac gcc ctt 672
His Ser Gly Asp Ala Ile Val Gly Tyr Leu Gln Gln Lys Tyr Ala Leu
210 215 220

aag aaa aat gca cac gca ttc cct aaa gtg gaa ttt cat gcg agc ggc 720
Lys Lys Asn Ala His Ala Phe Pro Lys Val Glu Phe His Ala Ser Gly
225 230 235 240

gat gtg atc tgg cta gaa aaa cag gct aaa gaa tgg ctc aaa ttg taa 768
Asp Val Ile Trp Leu Glu Lys Gln Ala Lys Glu Trp Leu Lys Leu *
245 250 255

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<210> 16
<211> 255
<212> PRT
<213> H. pylori

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1 5 10 15
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20 25 30
Asp Ser Ala Arg Val Pro Tyr Gly Thr Lys Asp Pro Thr Ile Lys
35 40 45
Gln Phe Gly Leu Glu Ala Leu Asp Phe Phe Lys Pro His Gln Ile Glu
50 55 60
Leu Leu Ile Val Ala Cys Asn Thr Ala Ser Ala Leu Ala Leu Glu Glu
65 70 75 80
Met Gln Lys His Ser Lys Ile Pro Ile Val Gly Val Ile Glu Pro Ser
85 90 95
Ile Leu Ala Ile Lys Gln Gln Val Lys Asp Lys Asn Ala Pro Ile Leu
100 105 110
Val Leu Gly Thr Lys Ala Thr Ile Gln Ser Asn Ala Tyr Asp Asn Ala
115 120 125
Leu Lys Gln Gln Gly Tyr Leu Asn Val Ser His Leu Ala Thr Ser Leu
130 135 140

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Phe Val Pro Leu Ile Glu Glu Ser Ile Leu Glu Gly Glu Leu Leu Glu  
 145 150 155 160  
 Thr Cys Met Arg Tyr Phe Thr Pro Leu Lys Ile Leu Pro Lys Val  
 165 170 175  
 Ile Ile Leu Gly Cys Thr His Phe Pro Leu Ile Ala His Gln Ile Lys  
 180 185 190  
 Gly Tyr Phe Met Gly His Phe Ala Leu Ser Thr Pro Pro Leu Leu Ile  
 195 200 205  
 His Ser Gly Asp Ala Ile Val Gly Tyr Leu Gln Gln Lys Tyr Ala Leu  
 210 215 220  
 Lys Lys Asn Ala His Ala Phe Pro Lys Val Glu Phe His Ala Ser Gly  
 225 230 235 240  
 Asp Val Ile Trp Leu Glu Lys Gln Ala Lys Glu Trp Leu Lys Leu  
 245 250 255

<210> 17  
 <211> 768  
 <212> DNA  
 <213> H. pylori

<220>  
 <221> CDS  
 <222> (1)...(768)

<400> 17  
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 Met Lys Ile Gly Val Phe Asp Ser Gly Val Gly Gly Phe Ser Val Leu  
 1 5 10 15  
  
 aaa agc ctt tta aaa gcg caa tta ttt gat gaa atc atc tat tat ggc 96  
 Lys Ser Leu Leu Lys Ala Gln Leu Phe Asp Glu Ile Ile Tyr Tyr Gly  
 20 25 30  
  
 gat agc gct aga gtg cct tat ggc act aaa gac ccc acc acg atc aag 144  
 Asp Ser Ala Arg Val Pro Tyr Gly Thr Lys Asp Pro Thr Thr Ile Lys  
 35 40 45  
  
 caa ttt ggc tta gag gct ttg gat ttt ttc aaa ccg cac cag att aaa 192  
 Gln Phe Gly Leu Glu Ala Leu Asp Phe Phe Lys Pro His Gln Ile Lys  
 50 55 60  
  
 tta ttg att gtg gca tgc aac aca gcg agt gct ctg gct tta gaa gag 240  
 Leu Leu Ile Val Ala Cys Asn Thr Ala Ser Ala Leu Ala Leu Glu Glu  
 65 70 75 80  
  
 atg caa aag cat tcc aaa atc cct att gtg ggc gtg att gag cca agc 288  
 Met Gln Lys His Ser Lys Ile Pro Ile Val Gly Val Ile Glu Pro Ser  
 85 90 95  
  
 att tta gcg atc aaa caa cag gta aaa gat aaa aac gcc ccc att tta 336  
 Ile Leu Ala Ile Lys Gln Gln Val Lys Asp Lys Asn Ala Pro Ile Leu  
 100 105 110  
  
 gtg cta ggc aca aaa gcg acg att caa tct aac gct tac gat aac gct 384  
 Val Leu Gly Thr Lys Ala Thr Ile Gln Ser Asn Ala Tyr Asp Asn Ala  
 115 120 125  
  
 ctg aaa cga caa ggc tat ttg aac gtt tcg cat tta gcc act tcc ctt 432

Leu	Lys	Arg	Gln	Gly	Tyr	Leu	Asn	Val	Ser	His	Leu	Ala	Thr	Ser	Leu		
130						135					140						
ttt	gtg	cct	ttg	att	gaa	gaa	agt	att	tta	gag	ggc	gaa	ttg	tta	gaa	480	
Phe	Val	Pro	Leu	Ile	Glu	Glu	Ser	Ile	Leu	Glu	Gly	Glu	Leu	Leu	Glu		
145					150					155					160		
act	tgc	atg	cgt	tat	tat	ttc	act	ccc	tta	aag	att	tta	cct	gaa	gtg	528	
Thr	Cys	Met	Arg	Tyr	Tyr	Phe	Thr	Pro	Leu	Lys	Ile	Leu	Pro	Glu	Val		
				165					170					175			
atc	att	tta	ggt	tgt	acg	cat	ttt	ccc	ttg	atc	gct	caa	aaa	att	gag	576	
Ile	Ile	Leu	Gly	Cys	Thr	His	Phe	Pro	Leu	Ile	Ala	Gln	Lys	Ile	Glu		
			180					185					190				
ggc	tat	ttt	atg	gaa	cat	ttt	gcc	ttt	cca	acg	ccc	ccc	cta	ctc	atc	624	
Gly	Tyr	Phe	Met	Glu	His	Phe	Ala	Phe	Pro	Thr	Pro	Pro	Leu	Leu	Ile		
		195					200					205					
cat	tcg	ggc	gat	gct	att	gtg	gaa	tat	ttg	cag	caa	aaa	tac	gcc	ctt	672	
His	Ser	Gly	Asp	Ala	Ile	Val	Glu	Tyr	Leu	Gln	Gln	Lys	Tyr	Ala	Leu		
		210				215					220						
aag	aaa	aat	gca	cac	gca	tta	cct	aaa	gtg	gaa	ttt	cat	gcg	agc	ggc	720	
Lys	Lys	Asn	Ala	His	Ala	Leu	Pro	Lys	Val	Glu	Phe	His	Ala	Ser	Gly		
225					230					235					240		
gat	gtg	atc	tgg	cta	gaa	aaa	caa	gct	aaa	gaa	tgg	ctc	aaa	ttg	taa	768	
Asp	Val	Ile	Trp	Leu	Glu	Lys	Gln	Ala	Lys	Glu	Trp	Leu	Lys	Leu	*		
				245					250					255			

<210> 18  
 <211> 255  
 <212> PRT  
 <213> H. pylori

<400> 18																	
Met	Lys	Ile	Gly	Val	Phe	Asp	Ser	Gly	Val	Gly	Gly	Phe	Ser	Val	Leu		
1				5					10					15			
Lys	Ser	Leu	Leu	Lys	Ala	Gln	Leu	Phe	Asp	Glu	Ile	Ile	Tyr	Tyr	Gly		
		20						25					30				
Asp	Ser	Ala	Arg	Val	Pro	Tyr	Gly	Thr	Lys	Asp	Pro	Thr	Thr	Ile	Lys		
		35					40					45					
Gln	Phe	Gly	Leu	Glu	Ala	Leu	Asp	Phe	Phe	Lys	Pro	His	Gln	Ile	Lys		
	50					55					60						
Leu	Leu	Ile	Val	Ala	Cys	Asn	Thr	Ala	Ser	Ala	Leu	Ala	Leu	Glu	Glu		
65					70					75				80			
Met	Gln	Lys	His	Ser	Lys	Ile	Pro	Ile	Val	Gly	Val	Ile	Glu	Pro	Ser		
			85						90				95				
Ile	Leu	Ala	Ile	Lys	Gln	Gln	Val	Lys	Asp	Lys	Asn	Ala	Pro	Ile	Leu		
		100						105					110				
Val	Leu	Gly	Thr	Lys	Ala	Thr	Ile	Gln	Ser	Asn	Ala	Tyr	Asp	Asn	Ala		
		115					120					125					
Leu	Lys	Arg	Gln	Gly	Tyr	Leu	Asn	Val	Ser	His	Leu	Ala	Thr	Ser	Leu		
		130				135					140						
Phe	Val	Pro	Leu	Ile	Glu	Glu	Ser	Ile	Leu	Glu	Gly	Glu	Leu	Leu	Glu		
145					150					155					160		

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Thr Cys Met Arg Tyr Tyr Phe Thr Pro Leu Lys Ile Leu Pro Glu Val
                                165                                170                                175
Ile Ile Leu Gly Cys Thr His Phe Pro Leu Ile Ala Gln Lys Ile Glu
                                180                                185                                190
Gly Tyr Phe Met Glu His Phe Ala Phe Pro Thr Pro Pro Leu Leu Ile
                                195                                200                                205
His Ser Gly Asp Ala Ile Val Glu Tyr Leu Gln Gln Lys Tyr Ala Leu
                                210                                215                                220
Lys Lys Asn Ala His Ala Leu Pro Lys Val Glu Phe His Ala Ser Gly
225                                230                                235                                240
Asp Val Ile Trp Leu Glu Lys Gln Ala Lys Glu Trp Leu Lys Leu
                                245                                250                                255

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<210> 19  
 <211> 768  
 <212> DNA  
 <213> H. pylori

<220>  
 <221> CDS  
 <222> (1)...(768)

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<400> 19
atg aaa ata ggc gtt ttt gat agc ggt gtg gga ggg ttt agc gtt tta 48
Met Lys Ile Gly Val Phe Asp Ser Gly Val Gly Gly Phe Ser Val Leu
  1                                5                                10                                15

aaa agc ctt tta aaa gcg caa tta ttt gat gaa atc atc tat tat ggc 96
Lys Ser Leu Leu Lys Ala Gln Leu Phe Asp Glu Ile Ile Tyr Tyr Gly
                                20                                25                                30

gat agc gct aga gtg cct tat ggc act aaa gac ccc acc acg atc aag 144
Asp Ser Ala Arg Val Pro Tyr Gly Thr Lys Asp Pro Thr Thr Ile Lys
                                35                                40                                45

caa ttt ggc tta gag gct ttg gat ttt ttc aaa ccg cac cag att aaa 192
Gln Phe Gly Leu Glu Ala Leu Asp Phe Phe Lys Pro His Gln Ile Lys
  50                                55                                60

tta ttg att gtg gca tgc aac aca gcg agc gct cta gct tta gaa gag 240
Leu Leu Ile Val Ala Cys Asn Thr Ala Ser Ala Leu Ala Leu Glu Glu
  65                                70                                75                                80

atg caa aag cat tcc aaa atc cct att gtg ggc gtg att gag cca agc 288
Met Gln Lys His Ser Lys Ile Pro Ile Val Gly Val Ile Glu Pro Ser
                                85                                90                                95

att tta gcg atc aaa caa caa gta aag gat aaa aac gcc ccc att tta 336
Ile Leu Ala Ile Lys Gln Gln Val Lys Asp Lys Asn Ala Pro Ile Leu
                                100                                105                                110

gtg cta ggg aca aaa gcg acg att caa tct aac gct tac gat aac gct 384
Val Leu Gly Thr Lys Ala Thr Ile Gln Ser Asn Ala Tyr Asp Asn Ala
                                115                                120                                125

ctg aaa caa caa ggc tat ttg aac gtt tcg cat tta gcc act tct ctt 432
Leu Lys Gln Gln Gly Tyr Leu Asn Val Ser His Leu Ala Thr Ser Leu
  130                                135                                140

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ttt gtg cct ttg att gaa gaa aat att tta gag ggc gaa ttg tta gaa 480
Phe Val Pro Leu Ile Glu Glu Asn Ile Leu Glu Gly Glu Leu Leu Glu
145          150          155          160

act tgc atg cgt tat tat ttc act ccc tta gag att tta cct gaa gtg 528
Thr Cys Met Arg Tyr Tyr Phe Thr Pro Leu Glu Ile Leu Pro Glu Val
          165          170          175

atc att tta ggt tgc acg cat ttt ccc tta atc gct caa aaa att gag 576
Ile Ile Leu Gly Cys Thr His Phe Pro Leu Ile Ala Gln Lys Ile Glu
          180          185          190

ggc tat ttc atg ggg cat ttt gcc ctt cca acg ccc ccc ata ctc atc 624
Gly Tyr Phe Met Gly His Phe Ala Leu Pro Thr Pro Pro Ile Leu Ile
          195          200          205

cat tct ggc gac gct att gta gaa tat ttg caa caa aaa tac gcc ctt 672
His Ser Gly Asp Ala Ile Val Glu Tyr Leu Gln Gln Lys Tyr Ala Leu
          210          215          220

aag aaa aat gca cac gca ttc cct aaa gtg gaa ttt cat gcg agc ggc 720
Lys Lys Asn Ala His Ala Phe Pro Lys Val Glu Phe His Ala Ser Gly
225          230          235          240

gat atg atc tgg cta gaa aaa caa gct aaa gaa tgg ctc aaa ttg taa 768
Asp Met Ile Trp Leu Glu Lys Gln Ala Lys Glu Trp Leu Lys Leu *
          245          250          255

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<210> 20  
 <211> 255  
 <212> PRT  
 <213> H. pylori

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<400> 20
Met Lys Ile Gly Val Phe Asp Ser Gly Val Gly Gly Phe Ser Val Leu
1      5      10      15
Lys Ser Leu Leu Lys Ala Gln Leu Phe Asp Glu Ile Ile Tyr Tyr Gly
20      25      30
Asp Ser Ala Arg Val Pro Tyr Gly Thr Lys Asp Pro Thr Thr Ile Lys
35      40      45
Gln Phe Gly Leu Glu Ala Leu Asp Phe Phe Lys Pro His Gln Ile Lys
50      55      60
Leu Leu Ile Val Ala Cys Asn Thr Ala Ser Ala Leu Ala Leu Glu Glu
65      70      75      80
Met Gln Lys His Ser Lys Ile Pro Ile Val Gly Val Ile Glu Pro Ser
85      90      95
Ile Leu Ala Ile Lys Gln Gln Val Lys Asp Lys Asn Ala Pro Ile Leu
100     105     110
Val Leu Gly Thr Lys Ala Thr Ile Gln Ser Asn Ala Tyr Asp Asn Ala
115     120     125
Leu Lys Gln Gln Gly Tyr Leu Asn Val Ser His Leu Ala Thr Ser Leu
130     135     140
Phe Val Pro Leu Ile Glu Asn Ile Leu Glu Gly Glu Leu Leu Glu
145     150     155     160
Thr Cys Met Arg Tyr Tyr Phe Thr Pro Leu Glu Ile Leu Pro Glu Val
          165          170          175

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Ile Ile Leu Gly Cys Thr His Phe Pro Leu Ile Ala Gln Lys Ile Glu
      180      185      190
Gly Tyr Phe Met Gly His Phe Ala Leu Pro Thr Pro Pro Ile Leu Ile
      195      200      205
His Ser Gly Asp Ala Ile Val Glu Tyr Leu Gln Gln Lys Tyr Ala Leu
      210      215      220
Lys Lys Asn Ala His Ala Phe Pro Lys Val Glu Phe His Ala Ser Gly
      225      230      235      240
Asp Met Ile Trp Leu Glu Lys Gln Ala Lys Glu Trp Leu Lys Leu
      245      250      255

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<210> 21  
 <211> 768  
 <212> DNA  
 <213> H. pylori

<220>  
 <221> CDS  
 <222> (1)...(768)

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<400> 21
atg aaa ata ggc gtt ttt gat agc ggt gtg gga ggg ttt agc gtt tta 48
Met Lys Ile Gly Val Phe Asp Ser Gly Val Gly Gly Phe Ser Val Leu
  1      5      10      15

aaa agc ctt tta aaa gcg caa tta ttt gat gaa atc atc tat tat ggc 96
Lys Ser Leu Leu Lys Ala Gln Leu Phe Asp Glu Ile Ile Tyr Tyr Gly
      20      25      30

gat agc gct aga gtg cct tat ggc act aaa gac ccc acc acg atc aag 144
Asp Ser Ala Arg Val Pro Tyr Gly Thr Lys Asp Pro Thr Thr Ile Lys
      35      40      45

caa ttt ggc tta gag gct ttg gat ttt ttc aaa ccg cac cag att aaa 192
Gln Phe Gly Leu Glu Ala Leu Asp Phe Phe Lys Pro His Gln Ile Lys
      50      55      60

tta ttg att gta gca tgc aac aca gcg agc gct cta gct tta gaa gag 240
Leu Leu Ile Val Ala Cys Asn Thr Ala Ser Ala Leu Ala Leu Glu Glu
      65      70      75      80

atg caa aag cat tcc aaa atc cct att gtg ggc gtg att gag cca agc 288
Met Gln Lys His Ser Lys Ile Pro Ile Val Gly Val Ile Glu Pro Ser
      85      90      95

att tta gcg atc aaa caa caa gta aaa gat aaa aac gcc cct att tta 336
Ile Leu Ala Ile Lys Gln Gln Val Lys Asp Lys Asn Ala Pro Ile Leu
      100      105      110

gtg cta ggg aca aaa gcg acg att caa tct aac gct tat gac aac gcc 384
Val Leu Gly Thr Lys Ala Thr Ile Gln Ser Asn Ala Tyr Asp Asn Ala
      115      120      125

ctg aaa caa caa ggc tat ttg aat gtt tcg cat tta gcc act tct ctt 432
Leu Lys Gln Gln Gly Tyr Leu Asn Val Ser His Leu Ala Thr Ser Leu
      130      135      140

ttt gtg cct ttg att gaa gaa agt att tta gag ggc gaa ttg tta gaa 480

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Phe	Val	Pro	Leu	Ile	Glu	Glu	Ser	Ile	Leu	Glu	Gly	Glu	Leu	Leu	Glu		
145					150					155					160		
act	tgc	atg	cgt	tat	tat	ttc	act	ccc	tta	aag	att	tta	cct	gaa	gtg	528	
Thr	Cys	Met	Arg	Tyr	Tyr	Phe	Thr	Pro	Leu	Lys	Ile	Leu	Pro	Glu	Val		
				165					170					175			
att	att	tta	ggt	tgc	acg	cat	ttt	ccc	ttg	atc	gct	caa	aaa	att	gag	576	
Ile	Ile	Leu	Gly	Cys	Thr	His	Phe	Pro	Leu	Ile	Ala	Gln	Lys	Ile	Glu		
			180					185					190				
agc	tat	ttt	atg	ggg	cat	ttt	gcc	ctt	cca	acg	ccc	ccc	cta	ctc	atc	624	
Ser	Tyr	Phe	Met	Gly	His	Phe	Ala	Leu	Pro	Thr	Pro	Pro	Leu	Leu	Ile		
		195					200					205					
cat	tct	ggc	gat	gct	att	gtg	gaa	tat	ttg	cag	caa	aaa	tac	gcc	ctt	672	
His	Ser	Gly	Asp	Ala	Ile	Val	Glu	Tyr	Leu	Gln	Gln	Lys	Tyr	Ala	Leu		
		210				215					220						
aag	aaa	aac	gca	cac	gca	ttc	cct	aaa	gtg	gaa	ttt	cat	gcg	agc	ggc	720	
Lys	Lys	Asn	Ala	His	Ala	Phe	Pro	Lys	Val	Glu	Phe	His	Ala	Ser	Gly		
225					230					235					240		
gat	gtg	atc	tgg	cta	gaa	aaa	caa	gct	aaa	gaa	tgg	ctc	aaa	ttg	taa	768	
Asp	Val	Ile	Trp	Leu	Glu	Lys	Gln	Ala	Lys	Glu	Trp	Leu	Lys	Leu	*		
				245					250					255			

<210> 22  
 <211> 255  
 <212> PRT  
 <213> H. pylori

<400> 22																	
Met	Lys	Ile	Gly	Val	Phe	Asp	Ser	Gly	Val	Gly	Gly	Phe	Ser	Val	Leu		
1				5					10					15			
Lys	Ser	Leu	Leu	Lys	Ala	Gln	Leu	Phe	Asp	Glu	Ile	Ile	Tyr	Tyr	Gly		
		20						25					30				
Asp	Ser	Ala	Arg	Val	Pro	Tyr	Gly	Thr	Lys	Asp	Pro	Thr	Thr	Ile	Lys		
		35					40					45					
Gln	Phe	Gly	Leu	Glu	Ala	Leu	Asp	Phe	Phe	Lys	Pro	His	Gln	Ile	Lys		
	50					55					60						
Leu	Leu	Ile	Val	Ala	Cys	Asn	Thr	Ala	Ser	Ala	Leu	Ala	Leu	Glu	Glu		
65					70					75					80		
Met	Gln	Lys	His	Ser	Lys	Ile	Pro	Ile	Val	Gly	Val	Ile	Glu	Pro	Ser		
			85						90					95			
Ile	Leu	Ala	Ile	Lys	Gln	Gln	Val	Lys	Asp	Lys	Asn	Ala	Pro	Ile	Leu		
			100					105					110				
Val	Leu	Gly	Thr	Lys	Ala	Thr	Ile	Gln	Ser	Asn	Ala	Tyr	Asp	Asn	Ala		
		115					120					125					
Leu	Lys	Gln	Gln	Gly	Tyr	Leu	Asn	Val	Ser	His	Leu	Ala	Thr	Ser	Leu		
		130				135					140						
Phe	Val	Pro	Leu	Ile	Glu	Glu	Ser	Ile	Leu	Glu	Gly	Glu	Leu	Leu	Glu		
145					150					155					160		
Thr	Cys	Met	Arg	Tyr	Tyr	Phe	Thr	Pro	Leu	Lys	Ile	Leu	Pro	Glu	Val		
				165					170					175			
Ile	Ile	Leu	Gly	Cys	Thr	His	Phe	Pro	Leu	Ile	Ala	Gln	Lys	Ile	Glu		
			180					185					190				

Ser	Tyr	Phe	Met	Gly	His	Phe	Ala	Leu	Pro	Thr	Pro	Pro	Leu	Leu	Ile
		195					200					205			
His	Ser	Gly	Asp	Ala	Ile	Val	Glu	Tyr	Leu	Gln	Gln	Lys	Tyr	Ala	Leu
	210					215					220				
Lys	Lys	Asn	Ala	His	Ala	Phe	Pro	Lys	Val	Glu	Phe	His	Ala	Ser	Gly
225					230					235					240
Asp	Val	Ile	Trp	Leu	Glu	Lys	Gln	Ala	Lys	Glu	Trp	Leu	Lys	Leu	
				245					250					255	

<210> 23  
 <211> 768  
 <212> DNA  
 <213> H. pylori

<220>  
 <221> CDS  
 <222> (1)...(768)

<400> 23																
atg	aaa	ata	ggc	gtt	ttt	gat	agc	ggt	gtg	gga	ggg	ttt	agc	gtt	tta	48
Met	Lys	Ile	Gly	Val	Phe	Asp	Ser	Gly	Val	Gly	Gly	Phe	Ser	Val	Leu	
1				5					10					15		
aaa agc ctt tta aaa gcg caa cta ttt gat gaa atc atc tat tat ggc															96	
Lys	Ser	Leu	Leu	Lys	Ala	Gln	Leu	Phe	Asp	Glu	Ile	Ile	Tyr	Tyr	Gly	
			20					25					30			
gat agc gct aga gtg cct tat ggc act aaa gac ccc acc acg atc aag															144	
Asp	Ser	Ala	Arg	Val	Pro	Tyr	Gly	Thr	Lys	Asp	Pro	Thr	Thr	Ile	Lys	
		35				40						45				
caa ttt ggc tta gag gct ttg gat ttt ttc aaa ccg cac cag att gga															192	
Gln	Phe	Gly	Leu	Glu	Ala	Leu	Asp	Phe	Phe	Lys	Pro	His	Gln	Ile	Gly	
		50				55					60					
tta ttg att gtg gca tgc aac aca gcg agc gct ctg gct tta gaa gag															240	
Leu	Leu	Ile	Val	Ala	Cys	Asn	Thr	Ala	Ser	Ala	Leu	Ala	Leu	Glu	Glu	
65					70				75					80		
atg caa aaa tat tcc aaa atc cct att gtg ggc gtg att gag cca agc															288	
Met	Gln	Lys	Tyr	Ser	Lys	Ile	Pro	Ile	Val	Gly	Val	Ile	Glu	Pro	Ser	
				85					90					95		
att tta gcg atc aaa caa caa gta aaa gat aaa aac gcc ccc att tta															336	
Ile	Leu	Ala	Ile	Lys	Gln	Gln	Val	Lys	Asp	Lys	Asn	Ala	Pro	Ile	Leu	
			100					105					110			
gtg cta ggg aca aaa gcg acg atc caa tct aac gct tat gat aac gcc															384	
Val	Leu	Gly	Thr	Lys	Ala	Thr	Ile	Gln	Ser	Asn	Ala	Tyr	Asp	Asn	Ala	
		115					120					125				
ctg aaa caa caa ggc tat ttg aac att tcg cat tta gcc act tct ctt															432	
Leu	Lys	Gln	Gln	Gly	Tyr	Leu	Asn	Ile	Ser	His	Leu	Ala	Thr	Ser	Leu	
		130				135					140					
ttt gtg ccc ttg att gaa gaa agt att tta gag ggc gaa ttg tta gaa															480	
Phe	Val	Pro	Leu	Ile	Glu	Glu	Ser	Ile	Leu	Glu	Gly	Glu	Leu	Leu	Glu	
145					150					155					160	

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act tgc atg cgt tat tat ttc act cca tta gag att tta cct gaa gtg 528
Thr Cys Met Arg Tyr Tyr Phe Thr Pro Leu Glu Ile Leu Pro Glu Val
                                165                                170                                175

atc att tta ggt tgc acg cat ttt ccc ttg atc gct caa aaa att gag 576
Ile Ile Leu Gly Cys Thr His Phe Pro Leu Ile Ala Gln Lys Ile Glu
                                180                                185                                190

agc tat ttt atg gag cat ttt gcc ctt tca acg ccc ccc tta ctc atc 624
Ser Tyr Phe Met Glu His Phe Ala Leu Ser Thr Pro Pro Leu Leu Ile
                                195                                200                                205

cat tct ggc gat gct att gtg gaa tac ttg caa caa aaa tac gcc ctt 672
His Ser Gly Asp Ala Ile Val Glu Tyr Leu Gln Gln Lys Tyr Ala Leu
                                210                                215                                220

aag aaa aac gca cac gca ttc cct aaa gtg gaa ttt cat gcg agc ggc 720
Lys Lys Asn Ala His Ala Phe Pro Lys Val Glu Phe His Ala Ser Gly
225                                230                                235                                240

gat gtg atc tgg cta gaa aaa cag gct aaa gaa tgg ctc aaa ttg taa 768
Asp Val Ile Trp Leu Glu Lys Gln Ala Lys Glu Trp Leu Lys Leu *
                                245                                250                                255

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<210> 24  
 <211> 255  
 <212> PRT  
 <213> H. pylori

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<400> 24
Met Lys Ile Gly Val Phe Asp Ser Gly Val Gly Gly Phe Ser Val Leu
 1      5      10      15
Lys Ser Leu Leu Lys Ala Gln Leu Phe Asp Glu Ile Ile Tyr Tyr Gly
 20      25
Asp Ser Ala Arg Val Pro Tyr Gly Thr Lys Asp Pro Thr Thr Ile Lys
 35      40      45
Gln Phe Gly Leu Glu Ala Leu Asp Phe Phe Lys Pro His Gln Ile Gly
 50      55      60
Leu Leu Ile Val Ala Cys Asn Thr Ala Ser Ala Leu Ala Leu Glu Glu
 65      70      75      80
Met Gln Lys Tyr Ser Lys Ile Pro Ile Val Gly Val Ile Glu Pro Ser
 85      90      95
Ile Leu Ala Ile Lys Gln Gln Val Lys Asp Lys Asn Ala Pro Ile Leu
100      105      110
Val Leu Gly Thr Lys Ala Thr Ile Gln Ser Asn Ala Tyr Asp Asn Ala
115      120      125
Leu Lys Gln Gln Gly Tyr Leu Asn Ile Ser His Leu Ala Thr Ser Leu
130      135      140
Phe Val Pro Leu Ile Glu Glu Ser Ile Leu Glu Gly Glu Leu Leu Glu
145      150      155      160
Thr Cys Met Arg Tyr Tyr Phe Thr Pro Leu Glu Ile Leu Pro Glu Val
165      170      175
Ile Ile Leu Gly Cys Thr His Phe Pro Leu Ile Ala Gln Lys Ile Glu
180      185      190
Ser Tyr Phe Met Glu His Phe Ala Leu Ser Thr Pro Pro Leu Leu Ile
195      200      205

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His	Ser	Gly	Asp	Ala	Ile	Val	Glu	Tyr	Leu	Gln	Gln	Lys	Tyr	Ala	Leu
	210					215				220					
Lys	Lys	Asn	Ala	His	Ala	Phe	Pro	Lys	Val	Glu	Phe	His	Ala	Ser	Gly
225					230					235					240
Asp	Val	Ile	Trp	Leu	Glu	Lys	Gln	Ala	Lys	Glu	Trp	Leu	Lys	Leu	
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 <212> DNA  
 <213> H. pylori

<220>  
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Met	Lys	Ile	Gly	Val	Phe	Asp	Ser	Gly	Val	Gly	Gly	Phe	Ser	Val	Leu	
1				5					10					15		
aaa agc ctt tta aaa gcg caa tta ttt gat gaa atc atc tat tat ggc															96	
Lys	Ser	Leu	Leu	Lys	Ala	Gln	Leu	Phe	Asp	Glu	Ile	Ile	Tyr	Tyr	Gly	
			20					25					30			
gat agc gct aga gtg cct tat ggc act aaa gac ccc acc acg atc aag															144	
Asp	Ser	Ala	Arg	Val	Pro	Tyr	Gly	Thr	Lys	Asp	Pro	Thr	Thr	Ile	Lys	
			35				40					45				
caa ttt ggc tta gag gct ttg gat ttt ttc aaa ccg cac aaa att gaa															192	
Gln	Phe	Gly	Leu	Glu	Ala	Leu	Asp	Phe	Phe	Lys	Pro	His	Lys	Ile	Glu	
		50				55					60					
tta tta att gtg gca tgc aac aca gcg agc gct ctg gct tta gaa gag															240	
Leu	Leu	Ile	Val	Ala	Cys	Asn	Thr	Ala	Ser	Ala	Leu	Ala	Leu	Glu	Glu	
	65				70				75					80		
atg caa aag cat tcc aaa atc ccc att gtg ggc gtg att gag cca agc															288	
Met	Gln	Lys	His	Ser	Lys	Ile	Pro	Ile	Val	Gly	Val	Ile	Glu	Pro	Ser	
				85					90					95		
att tta gcg atc aaa caa caa gtg aaa gat aaa aac acc cct att tta															336	
Ile	Leu	Ala	Ile	Lys	Gln	Gln	Val	Lys	Asp	Lys	Asn	Thr	Pro	Ile	Leu	
			100					105					110			
gtg cta ggg aca aaa gcg acg atc caa tct aac gct tac gat aac gcc															384	
Val	Leu	Gly	Thr	Lys	Ala	Thr	Ile	Gln	Ser	Asn	Ala	Tyr	Asp	Asn	Ala	
		115					120					125				
ctg aaa caa caa ggc tat ttg aag gtt tcg cat ttg gcc act tct ctt															432	
Leu	Lys	Gln	Gln	Gly	Tyr	Leu	Lys	Val	Ser	His	Leu	Ala	Thr	Ser	Leu	
		130				135					140					
ttt gtg cct ttg att gaa gaa agt att tta gag ggc gaa ttg tta gaa															480	
Phe	Val	Pro	Leu	Ile	Glu	Glu	Ser	Ile	Leu	Glu	Gly	Glu	Leu	Leu	Glu	
				150					155						160	
act tgc atg cgt tat tat ttc act cca tta gaa atc tta cct gaa gtg															528	

Thr	Cys	Met	Arg	Tyr	Tyr	Phe	Thr	Pro	Leu	Glu	Ile	Leu	Pro	Glu	Val		
				165					170					175			
gtt	att	tta	ggc	tgc	acg	cat	ttt	ccc	ttg	atc	gct	caa	aaa	att	gag	576	
Val	Ile	Leu	Gly	Cys	Thr	His	Phe	Pro	Leu	Ile	Ala	Gln	Lys	Ile	Glu		
			180					185					190				
ggc	tat	ttt	atg	gaa	cat	ttt	gcc	ctt	cca	acg	ccc	ccc	cta	ctc	atc	624	
Gly	Tyr	Phe	Met	Glu	His	Phe	Ala	Leu	Pro	Thr	Pro	Pro	Leu	Leu	Ile		
			195				200					205					
cat	tct	ggc	gac	gct	att	gtg	gga	tat	ttg	cag	caa	aaa	tac	gcc	ctt	672	
His	Ser	Gly	Asp	Ala	Ile	Val	Gly	Tyr	Leu	Gln	Gln	Lys	Tyr	Ala	Leu		
	210					215					220						
aag	aaa	aac	gca	cac	gca	ttc	cct	aaa	gtg	gaa	ttt	cat	gcg	agc	ggc	720	
Lys	Lys	Asn	Ala	His	Ala	Phe	Pro	Lys	Val	Glu	Phe	His	Ala	Ser	Gly		
225					230					235					240		
gat	gta	att	tgg	cta	gaa	aaa	cag	gct	aaa	gaa	tgg	ctc	aaa	ttg	taa	768	
Asp	Val	Ile	Trp	Leu	Glu	Lys	Gln	Ala	Lys	Glu	Trp	Leu	Lys	Leu	*		
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 <212> PRT  
 <213> H. pylori

<400> 26

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Lys	Ser	Leu	Leu	Lys	Ala	Gln	Leu	Phe	Asp	Glu	Ile	Ile	Tyr	Tyr	Gly		
			20					25					30				
Asp	Ser	Ala	Arg	Val	Pro	Tyr	Gly	Thr	Lys	Asp	Pro	Thr	Thr	Ile	Lys		
		35					40					45					
Gln	Phe	Gly	Leu	Glu	Ala	Leu	Asp	Phe	Phe	Lys	Pro	His	Lys	Ile	Glu		
	50					55					60						
Leu	Leu	Ile	Val	Ala	Cys	Asn	Thr	Ala	Ser	Ala	Leu	Ala	Leu	Glu	Glu		
65					70					75				80			
Met	Gln	Lys	His	Ser	Lys	Ile	Pro	Ile	Val	Gly	Val	Ile	Glu	Pro	Ser		
			85						90					95			
Ile	Leu	Ala	Ile	Lys	Gln	Gln	Val	Lys	Asp	Lys	Asn	Thr	Pro	Ile	Leu		
			100					105					110				
Val	Leu	Gly	Thr	Lys	Ala	Thr	Ile	Gln	Ser	Asn	Ala	Tyr	Asp	Asn	Ala		
		115					120					125					
Leu	Lys	Gln	Gln	Gly	Tyr	Leu	Lys	Val	Ser	His	Leu	Ala	Thr	Ser	Leu		
	130					135					140						
Phe	Val	Pro	Leu	Ile	Glu	Glu	Ser	Ile	Leu	Glu	Gly	Glu	Leu	Leu	Glu		
145					150					155				160			
Thr	Cys	Met	Arg	Tyr	Tyr	Phe	Thr	Pro	Leu	Glu	Ile	Leu	Pro	Glu	Val		
				165					170					175			
Val	Ile	Leu	Gly	Cys	Thr	His	Phe	Pro	Leu	Ile	Ala	Gln	Lys	Ile	Glu		
			180					185					190				
Gly	Tyr	Phe	Met	Glu	His	Phe	Ala	Leu	Pro	Thr	Pro	Pro	Leu	Leu	Ile		
		195					200					205					
His	Ser	Gly	Asp	Ala	Ile	Val	Gly	Tyr	Leu	Gln	Gln	Lys	Tyr	Ala	Leu		
	210					215					220						

Lys	Lys	Asn	Ala	His	Ala	Phe	Pro	Lys	Val	Glu	Phe	His	Ala	Ser	Gly
225					230					235					240
Asp	Val	Ile	Trp	Leu	Glu	Lys	Gln	Ala	Lys	Glu	Trp	Leu	Lys	Leu	
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<210> 27  
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 <212> DNA  
 <213> H. pylori

<220>  
 <221> CDS  
 <222> (1)...(768)

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Met	Lys	Ile	Gly	Val	Phe	Asp	Ser	Gly	Val	Gly	Gly	Phe	Ser	Val	Leu	
1				5					10					15		
aaa	agc	ctt	tta	aaa	gcg	caa	att	ttt	gat	gaa	atc	atc	tat	tat	ggc	96
Lys	Ser	Leu	Leu	Lys	Ala	Gln	Ile	Phe	Asp	Glu	Ile	Ile	Tyr	Tyr	Gly	
			20					25					30			
gat	agc	gct	agg	gtg	cct	tat	ggc	act	aaa	gac	ccc	acc	acg	atc	aag	144
Asp	Ser	Ala	Arg	Val	Pro	Tyr	Gly	Thr	Lys	Asp	Pro	Thr	Thr	Ile	Lys	
		35					40					45				
caa	ttt	ggc	tta	gag	gct	ttg	gat	ttt	ttc	aaa	ccg	cac	aag	att	gaa	192
Gln	Phe	Gly	Leu	Glu	Ala	Leu	Asp	Phe	Phe	Lys	Pro	His	Lys	Ile	Glu	
	50					55					60					
tta	ttg	att	gtg	gca	tgc	aac	aca	gcg	agc	gct	cta	gct	tta	gaa	gaa	240
Leu	Leu	Ile	Val	Ala	Cys	Asn	Thr	Ala	Ser	Ala	Leu	Ala	Leu	Glu	Glu	
65					70				75					80		
atg	caa	aag	cat	tcc	aaa	atc	cct	att	gtg	ggc	gtg	att	gaa	cca	agc	288
Met	Gln	Lys	His	Ser	Lys	Ile	Pro	Ile	Val	Gly	Val	Ile	Glu	Pro	Ser	
				85					90					95		
att	tta	gcg	atc	aaa	caa	caa	gta	aaa	gat	aaa	aac	gcc	cct	att	tta	336
Ile	Leu	Ala	Ile	Lys	Gln	Gln	Val	Lys	Asp	Lys	Asn	Ala	Pro	Ile	Leu	
			100					105					110			
gtg	cta	ggg	aca	aaa	gcg	acg	att	caa	tct	aac	gct	tat	gac	aac	gcc	384
Val	Leu	Gly	Thr	Lys	Ala	Thr	Ile	Gln	Ser	Asn	Ala	Tyr	Asp	Asn	Ala	
		115					120					125				
ctg	aaa	caa	caa	ggc	tat	ttg	aat	gtt	tcg	cat	tta	gcc	act	tct	ott	432
Leu	Lys	Gln	Gln	Gly	Tyr	Leu	Asn	Val	Ser	His	Leu	Ala	Thr	Ser	Leu	
	130					135					140					
ttt	gtg	cct	ttg	att	gaa	gaa	aat	att	tta	gag	ggc	gaa	ttg	cta	gaa	480
Phe	Val	Pro	Leu	Ile	Glu	Glu	Asn	Ile	Leu	Glu	Gly	Glu	Leu	Leu	Glu	
145					150					155					160	
act	tgc	atg	cgt	tat	tat	ttc	act	cca	tta	gag	atc	ttg	cct	gaa	gtg	528
Thr	Cys	Met	Arg	Tyr	Tyr	Phe	Thr	Pro	Leu	Glu	Ile	Leu	Pro	Glu	Val	
				165					170					175		

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gtt att tta ggc tgc acg cat ttt ccc ttg atc gct cac caa att gag 576
Val Ile Leu Gly Cys Thr His Phe Pro Leu Ile Ala His Gln Ile Glu
               180               185               190

ggc tat ttt atg gag cat ttt gcc ctt tca acg ccc ccc cta ctc atc 624
Gly Tyr Phe Met Glu His Phe Ala Leu Ser Thr Pro Pro Leu Leu Ile
               195               200               205

cat tct ggc gat gct att gtg gaa tat ttg cag caa aaa tac gcc ctt 672
His Ser Gly Asp Ala Ile Val Glu Tyr Leu Gln Gln Lys Tyr Ala Leu
               210               215               220

aag aaa aac gca tgt gca ttc cct aaa gta gaa ttt cat gcg agc ggc 720
Lys Lys Asn Ala Cys Ala Phe Pro Lys Val Glu Phe His Ala Ser Gly
225               230               235               240

gat gta att tgg cta gaa aaa cag gct aaa gaa tgg ctc aaa ttg taa 768
Asp Val Ile Trp Leu Glu Lys Gln Ala Lys Glu Trp Leu Lys Leu *
               245               250               255

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<210> 28  
 <211> 255  
 <212> PRT  
 <213> H. pylori

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 1      5      10      15
Lys Ser Leu Leu Lys Ala Gln Ile Phe Asp Glu Ile Ile Tyr Tyr Gly
20      25      30
Asp Ser Ala Arg Val Pro Tyr Gly Thr Lys Asp Pro Thr Thr Ile Lys
35      40      45
Gln Phe Gly Leu Glu Ala Leu Asp Phe Phe Lys Pro His Lys Ile Glu
50      55      60
Leu Leu Ile Val Ala Cys Asn Thr Ala Ser Ala Leu Ala Leu Glu Glu
65      70      75      80
Met Gln Lys His Ser Lys Ile Pro Ile Val Gly Val Ile Glu Pro Ser
85      90      95
Ile Leu Ala Ile Lys Gln Gln Val Lys Asp Lys Asn Ala Pro Ile Leu
100     105     110
Val Leu Gly Thr Lys Ala Thr Ile Gln Ser Asn Ala Tyr Asp Asn Ala
115     120     125
Leu Lys Gln Gln Gly Tyr Leu Asn Val Ser His Leu Ala Thr Ser Leu
130     135     140
Phe Val Pro Leu Ile Glu Glu Asn Ile Leu Glu Gly Glu Leu Leu Glu
145     150     155     160
Thr Cys Met Arg Tyr Tyr Phe Thr Pro Leu Glu Ile Leu Pro Glu Val
165     170     175
Val Ile Leu Gly Cys Thr His Phe Pro Leu Ile Ala His Gln Ile Glu
180     185     190
Gly Tyr Phe Met Glu His Phe Ala Leu Ser Thr Pro Pro Leu Leu Ile
195     200     205
His Ser Gly Asp Ala Ile Val Glu Tyr Leu Gln Gln Lys Tyr Ala Leu
210     215     220
Lys Lys Asn Ala Cys Ala Phe Pro Lys Val Glu Phe His Ala Ser Gly
225     230     235     240

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Asp Val Ile Trp Leu Glu Lys Gln Ala Lys Glu Trp Leu Lys Leu  
 245 250 255

<210> 29  
 <211> 768  
 <212> DNA  
 <213> H. pylori

<220>  
 <221> CDS  
 <222> (1)...(768)

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 Met Lys Ile Gly Val Phe Asp Ser Gly Val Gly Gly Phe Ser Val Leu  
 1 5 10 15

aaa agc ctt tta aaa gtg caa tta ttt gat gaa atc atc tat tat ggc 96  
 Lys Ser Leu Leu Lys Val Gln Leu Phe Asp Glu Ile Ile Tyr Tyr Gly  
 20 25 30

gat agt gct agg gtg cct tat ggc act aaa gac ccc acc acg atc aag 144  
 Asp Ser Ala Arg Val Pro Tyr Gly Thr Lys Asp Pro Thr Thr Ile Lys  
 35 40 45

caa ttt ggc tta gag gct ttg gat ttt ttc aaa ccg cac aag att gaa 192  
 Gln Phe Gly Leu Glu Ala Leu Asp Phe Phe Lys Pro His Lys Ile Glu  
 50 55 60

tta ttg att gtg gca tgc aac aca gcg agc gct cta gct tta gga gag 240  
 Leu Leu Ile Val Ala Cys Asn Thr Ala Ser Ala Leu Ala Leu Gly Glu  
 65 70 75 80

atg caa aag tat tcc aaa atc cct att gtg ggc gtg att gag cca agc 288  
 Met Gln Lys Tyr Ser Lys Ile Pro Ile Val Gly Val Ile Glu Pro Ser  
 85 90 95

att tta gcg atc aaa caa caa gta aaa gat aaa aac gcc cct att tta 336  
 Ile Leu Ala Ile Lys Gln Gln Val Lys Asp Lys Asn Ala Pro Ile Leu  
 100 105 110

gta cta ggg aca aaa gcg acg att cga tcc aac gct tat gac aac gcc 384  
 Val Leu Gly Thr Lys Ala Thr Ile Arg Ser Asn Ala Tyr Asp Asn Ala  
 115 120 125

ctg aaa caa caa ggc tat ttg aat att tcg cat tta gcc act tct ctt 432  
 Leu Lys Gln Gln Gly Tyr Leu Asn Ile Ser His Leu Ala Thr Ser Leu  
 130 135 140

ttt gtg cct ttg att gaa gaa aat att tta gag ggc gaa ttg cta gaa 480  
 Phe Val Pro Leu Ile Glu Glu Asn Ile Leu Glu Gly Glu Leu Leu Glu  
 145 150 155 160

act tgc atg cgt tat tat ttc act cca tta gag att tta cct gaa gtg 528  
 Thr Cys Met Arg Tyr Tyr Phe Thr Pro Leu Glu Ile Leu Pro Glu Val  
 165 170 175

gtt att tta ggt tgc acg cat ttt ccc ttg atc gct cac caa att gag 576

Val	Ile	Leu	Gly	Cys	Thr	His	Phe	Pro	Leu	Ile	Ala	His	Gln	Ile	Glu		
			180					185					190				
ggc	tat	ttt	atg	gag	cat	ttt	gcc	ctt	tca	acg	ccc	ccc	cta	ctc	atc	624	
Gly	Tyr	Phe	Met	Glu	His	Phe	Ala	Leu	Ser	Thr	Pro	Pro	Leu	Leu	Ile		
		195					200				205						
cat	tct	ggc	gat	gct	att	gtg	gaa	tat	ttg	caa	caa	aaa	tac	gcc	ctt	672	
His	Ser	Gly	Asp	Ala	Ile	Val	Glu	Tyr	Leu	Gln	Gln	Lys	Tyr	Ala	Leu		
	210					215				220							
aag	aaa	aac	gca	tgc	gca	ttc	cct	aaa	gta	gaa	ttc	cat	gcg	agc	ggc	720	
Lys	Lys	Asn	Ala	Cys	Ala	Phe	Pro	Lys	Val	Glu	Phe	His	Ala	Ser	Gly		
225				230					235						240		
gat	gta	att	tgg	cta	gaa	aaa	cag	gct	aaa	gaa	tgg	ctc	aaa	ttg	taa	768	
Asp	Val	Ile	Trp	Leu	Glu	Lys	Gln	Ala	Lys	Glu	Trp	Leu	Lys	Leu	*		
			245					250						255			

<210> 30  
 <211> 255  
 <212> PRT  
 <213> H. pylori

<400> 30

Met	Lys	Ile	Gly	Val	Phe	Asp	Ser	Gly	Val	Gly	Gly	Phe	Ser	Val	Leu		
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Lys	Ser	Leu	Leu	Lys	Val	Gln	Leu	Phe	Asp	Glu	Ile	Ile	Tyr	Tyr	Gly		
		20						25					30				
Asp	Ser	Ala	Arg	Val	Pro	Tyr	Gly	Thr	Lys	Asp	Pro	Thr	Thr	Ile	Lys		
		35					40					45					
Gln	Phe	Gly	Leu	Glu	Ala	Leu	Asp	Phe	Phe	Lys	Pro	His	Lys	Ile	Glu		
	50					55					60						
Leu	Leu	Ile	Val	Ala	Cys	Asn	Thr	Ala	Ser	Ala	Leu	Ala	Leu	Gly	Glu		
65					70				75					80			
Met	Gln	Lys	Tyr	Ser	Lys	Ile	Pro	Ile	Val	Gly	Val	Ile	Glu	Pro	Ser		
			85						90					95			
Ile	Leu	Ala	Ile	Lys	Gln	Gln	Val	Lys	Asp	Lys	Asn	Ala	Pro	Ile	Leu		
		100						105					110				
Val	Leu	Gly	Thr	Lys	Ala	Thr	Ile	Arg	Ser	Asn	Ala	Tyr	Asp	Asn	Ala		
		115					120					125					
Leu	Lys	Gln	Gln	Gly	Tyr	Leu	Asn	Ile	Ser	His	Leu	Ala	Thr	Ser	Leu		
		130				135					140						
Phe	Val	Pro	Leu	Ile	Glu	Glu	Asn	Ile	Leu	Glu	Gly	Glu	Leu	Leu	Glu		
145					150					155					160		
Thr	Cys	Met	Arg	Tyr	Tyr	Phe	Thr	Pro	Leu	Glu	Ile	Leu	Pro	Glu	Val		
			165						170					175			
Val	Ile	Leu	Gly	Cys	Thr	His	Phe	Pro	Leu	Ile	Ala	His	Gln	Ile	Glu		
		180						185					190				
Gly	Tyr	Phe	Met	Glu	His	Phe	Ala	Leu	Ser	Thr	Pro	Pro	Leu	Leu	Ile		
		195					200					205					
His	Ser	Gly	Asp	Ala	Ile	Val	Glu	Tyr	Leu	Gln	Gln	Lys	Tyr	Ala	Leu		
	210					215					220						
Lys	Lys	Asn	Ala	Cys	Ala	Phe	Pro	Lys	Val	Glu	Phe	His	Ala	Ser	Gly		
225				230						235					240		
Asp	Val	Ile	Trp	Leu	Glu	Lys	Gln	Ala	Lys	Glu	Trp	Leu	Lys	Leu			
			245					250						255			

<210> 31  
 <211> 768  
 <212> DNA  
 <213> H. pylori

<220>  
 <221> CDS  
 <222> (1)...(768)

<400> 31

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Met	Lys	Ile	Gly	Val	Phe	Asp	Ser	Gly	Val	Gly	Gly	Phe	Ser	Val	Leu	
1				5					10					15		
aaa	agc	ctt	tta	aaa	gcg	caa	att	ttt	gat	gaa	atc	atc	tat	tat	ggc	96
Lys	Ser	Leu	Leu	Lys	Ala	Gln	Ile	Phe	Asp	Glu	Ile	Ile	Tyr	Tyr	Gly	
			20					25					30			
gat	agt	gct	aga	gtg	cct	tat	ggc	act	aaa	gac	ccc	acc	acg	atc	aag	144
Asp	Ser	Ala	Arg	Val	Pro	Tyr	Gly	Thr	Lys	Asp	Pro	Thr	Thr	Ile	Lys	
			35				40					45				
caa	ttt	ggc	tta	gag	gct	ttg	gat	ttt	ttc	aaa	ccg	cac	cag	att	gga	192
Gln	Phe	Gly	Leu	Glu	Ala	Leu	Asp	Phe	Phe	Lys	Pro	His	Gln	Ile	Gly	
		50				55					60					
tta	ttg	att	gtg	gca	tgc	aac	aca	gcg	agc	gct	cta	gct	tta	gaa	gag	240
Leu	Leu	Ile	Val	Ala	Cys	Asn	Thr	Ala	Ser	Ala	Leu	Ala	Leu	Glu	Glu	
	65				70				75					80		
atg	caa	aag	cat	tcc	aaa	atc	cct	att	gtg	ggt	gtg	att	gag	cca	agc	288
Met	Gln	Lys	His	Ser	Lys	Ile	Pro	Ile	Val	Gly	Val	Ile	Glu	Pro	Ser	
				85					90				95			
att	tta	gcg	atc	aaa	caa	caa	gta	aaa	gat	aaa	aac	gcc	cct	att	tta	336
Ile	Leu	Ala	Ile	Lys	Gln	Gln	Val	Lys	Asp	Lys	Asn	Ala	Pro	Ile	Leu	
			100					105					110			
gtg	tta	ggg	aca	aaa	gcg	acg	att	caa	tcc	aac	gct	tat	gac	aac	gcc	384
Val	Leu	Gly	Thr	Lys	Ala	Thr	Ile	Gln	Ser	Asn	Ala	Tyr	Asp	Asn	Ala	
		115					120					125				
ctg	aaa	caa	caa	ggc	tat	ttg	aac	ggt	tcg	cat	tta	gcc	act	tct	ctt	432
Leu	Lys	Gln	Gln	Gly	Tyr	Leu	Asn	Val	Ser	His	Leu	Ala	Thr	Ser	Leu	
	130					135					140					
ttt	gtg	cct	ttg	att	gaa	gaa	aat	att	tta	gag	ggc	gaa	ttg	tta	gaa	480
Phe	Val	Pro	Leu	Ile	Glu	Glu	Asn	Ile	Leu	Glu	Gly	Glu	Leu	Leu	Glu	
	145				150				155					160		
act	tgc	atg	cgt	tat	tat	ttc	act	cca	tta	gag	att	tta	cct	gaa	gtg	528
Thr	Cys	Met	Arg	Tyr	Tyr	Phe	Thr	Pro	Leu	Glu	Ile	Leu	Pro	Glu	Val	
				165				170					175			
ggt	att	tta	ggt	tgc	acg	cat	ttt	ccc	ttg	atc	gct	cac	caa	att	gag	576
Val	Ile	Leu	Gly	Cys	Thr	His	Phe	Pro	Leu	Ile	Ala	His	Gln	Ile	Glu	
			180					185					190			

ggc	tat	ttt	atg	gag	cat	ttt	gcc	ctt	tca	acg	ccc	ccc	tta	ctc	atc	624
Gly	Tyr	Phe	Met	Glu	His	Phe	Ala	Leu	Ser	Thr	Pro	Pro	Leu	Leu	Ile	
		195					200					205				
cat	tct	ggc	gat	gct	att	gtg	gaa	tat	ttg	caa	caa	aaa	tac	acc	ctt	672
His	Ser	Gly	Asp	Ala	Ile	Val	Glu	Tyr	Leu	Gln	Gln	Lys	Tyr	Thr	Leu	
	210					215					220					
aag	aaa	aat	gca	tgc	gcg	ttc	cct	aaa	gtg	gaa	ttt	cat	gcg	agc	ggc	720
Lys	Lys	Asn	Ala	Cys	Ala	Phe	Pro	Lys	Val	Glu	Phe	His	Ala	Ser	Gly	
225					230					235					240	
gat	gtg	gtt	tgg	cta	gaa	aaa	cag	gct	aaa	gaa	tgg	ctc	aaa	ttg	taa	768
Asp	Val	Val	Trp	Leu	Glu	Lys	Gln	Ala	Lys	Glu	Trp	Leu	Lys	Leu	*	
				245					250					255		

<210> 32  
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 <212> PRT  
 <213> H. pylori

<400> 32

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		20						25					30			
Asp	Ser	Ala	Arg	Val	Pro	Tyr	Gly	Thr	Lys	Asp	Pro	Thr	Thr	Ile	Lys	
		35					40					45				
Gln	Phe	Gly	Leu	Glu	Ala	Leu	Asp	Phe	Phe	Lys	Pro	His	Gln	Ile	Gly	
	50					55					60					
Leu	Leu	Ile	Val	Ala	Cys	Asn	Thr	Ala	Ser	Ala	Leu	Ala	Leu	Glu	Glu	
65					70					75					80	
Met	Gln	Lys	His	Ser	Lys	Ile	Pro	Ile	Val	Gly	Val	Ile	Glu	Pro	Ser	
			85						90					95		
Ile	Leu	Ala	Ile	Lys	Gln	Gln	Val	Lys	Asp	Lys	Asn	Ala	Pro	Ile	Leu	
		100						105					110			
Val	Leu	Gly	Thr	Lys	Ala	Thr	Ile	Gln	Ser	Asn	Ala	Tyr	Asp	Asn	Ala	
		115					120					125				
Leu	Lys	Gln	Gln	Gly	Tyr	Leu	Asn	Val	Ser	His	Leu	Ala	Thr	Ser	Leu	
	130					135					140					
Phe	Val	Pro	Leu	Ile	Glu	Glu	Asn	Ile	Leu	Glu	Gly	Glu	Leu	Leu	Glu	
145					150					155					160	
Thr	Cys	Met	Arg	Tyr	Tyr	Phe	Thr	Pro	Leu	Glu	Ile	Leu	Pro	Glu	Val	
			165					170						175		
Val	Ile	Leu	Gly	Cys	Thr	His	Phe	Pro	Leu	Ile	Ala	His	Gln	Ile	Glu	
		180						185					190			
Gly	Tyr	Phe	Met	Glu	His	Phe	Ala	Leu	Ser	Thr	Pro	Pro	Leu	Leu	Ile	
		195					200					205				
His	Ser	Gly	Asp	Ala	Ile	Val	Glu	Tyr	Leu	Gln	Gln	Lys	Tyr	Thr	Leu	
	210					215					220					
Lys	Lys	Asn	Ala	Cys	Ala	Phe	Pro	Lys	Val	Glu	Phe	His	Ala	Ser	Gly	
225					230					235					240	
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				245					250					255		

<210> 33



<211> 765  
 <212> DNA  
 <213> H. pylori

<220>  
 <221> CDS  
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<400> 33

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Met	Lys	Ile	Gly	Val	Phe	Asp	Ser	Gly	Val	Gly	Gly	Phe	Ser	Val	Leu	
1				5					10					15		
aaa	agc	ctt	tta	aaa	gcg	caa	cta	ttt	gat	gaa	atc	atc	tat	tat	ggc	96
Lys	Ser	Leu	Leu	Lys	Ala	Gln	Leu	Phe	Asp	Glu	Ile	Ile	Tyr	Tyr	Gly	
			20					25					30			
gat	agc	gct	aga	gtg	cct	tat	ggc	act	aaa	gac	ccc	acc	acg	atc	aag	144
Asp	Ser	Ala	Arg	Val	Pro	Tyr	Gly	Thr	Lys	Asp	Pro	Thr	Thr	Ile	Lys	
			35				40					45				
caa	ttt	ggc	tta	gag	gct	ttg	gat	ttt	ttc	aaa	ccg	cac	cag	att	aaa	192
Gln	Phe	Gly	Leu	Glu	Ala	Leu	Asp	Phe	Phe	Lys	Pro	His	Gln	Ile	Lys	
	50					55					60					
tta	ttg	att	gtg	gca	tgc	aac	acc	gca	agc	gct	ctg	gct	tta	gaa	gag	240
Leu	Leu	Ile	Val	Ala	Cys	Asn	Thr	Ala	Ser	Ala	Leu	Ala	Leu	Glu	Glu	
	65				70				75					80		
atg	caa	aag	cat	tcc	aaa	atc	cct	gtt	gtg	ggc	gtg	att	gag	cca	agc	288
Met	Gln	Lys	His	Ser	Lys	Ile	Pro	Val	Val	Gly	Val	Ile	Glu	Pro	Ser	
				85					90					95		
att	tta	gcg	atc	aaa	cgg	caa	gtg	aaa	gat	aaa	aac	gcc	cct	att	ttg	336
Ile	Leu	Ala	Ile	Lys	Arg	Gln	Val	Lys	Asp	Lys	Asn	Ala	Pro	Ile	Leu	
			100					105					110			
gtg	cta	ggg	aca	aaa	gcg	acg	att	caa	tcc	aac	gcc	tat	gat	aac	gcc	384
Val	Leu	Gly	Thr	Lys	Ala	Thr	Ile	Gln	Ser	Asn	Ala	Tyr	Asp	Asn	Ala	
		115					120					125				
ctg	aaa	caa	caa	ggc	tat	ttg	aat	gtt	tcg	cat	tta	gcc	act	tct	ctt	432
Leu	Lys	Gln	Gln	Gly	Tyr	Leu	Asn	Val	Ser	His	Leu	Ala	Thr	Ser	Leu	
	130					135					140					
ttt	gtg	cct	ttg	att	gaa	gaa	agt	att	tta	gag	ggc	gaa	ttg	cta	gaa	480
Phe	Val	Pro	Leu	Ile	Glu	Glu	Ser	Ile	Leu	Glu	Gly	Glu	Leu	Leu	Glu	
	145				150				155					160		
act	tgc	atg	cgt	tat	tat	ttc	act	cca	tta	gag	att	tta	cct	gaa	gtg	528
Thr	Cys	Met	Arg	Tyr	Tyr	Phe	Thr	Pro	Leu	Glu	Ile	Leu	Pro	Glu	Val	
				165				170						175		
gtt	att	tta	ggg	tgc	acg	cat	ttt	ccc	ttg	atc	gct	caa	aaa	att	gag	576
Val	Ile	Leu	Gly	Cys	Thr	His	Phe	Pro	Leu	Ile	Ala	Gln	Lys	Ile	Glu	
			180					185					190			
ggc	tat	ttt	atg	gag	cat	ttt	gcc	ctt	tca	acg	ccc	ccc	cta	ctc	atc	624

Gly	Tyr	Phe	Met	Glu	His	Phe	Ala	Leu	Ser	Thr	Pro	Pro	Leu	Leu	Ile		
		195					200					205					
cat	tct	ggc	gat	gct	att	gtg	gaa	tat	ttg	caa	caa	aat	tac	gcc	ctt	672	
His	Ser	Gly	Asp	Ala	Ile	Val	Glu	Tyr	Leu	Gln	Gln	Asn	Tyr	Ala	Leu		
	210					215					220						
aag	aaa	aac	gca	tgc	gcg	ttc	cct	aaa	gtg	gaa	ttt	cat	gcg	agc	ggc	720	
Lys	Lys	Asn	Ala	Cys	Ala	Phe	Pro	Lys	Val	Glu	Phe	His	Ala	Ser	Gly		
225					230					235					240		
gat	gtg	gtt	tgg	cta	gaa	aaa	caa	gct	aaa	gaa	tgg	ctt	aaa	ttg		765	
Asp	Val	Val	Trp	Leu	Glu	Lys	Gln	Ala	Lys	Glu	Trp	Leu	Lys	Leu			
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<210> 34  
 <211> 255  
 <212> PRT  
 <213> H. pylori

<400> 34

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Lys	Ser	Leu	Leu	Lys	Ala	Gln	Leu	Phe	Asp	Glu	Ile	Ile	Tyr	Tyr	Gly		
		20						25					30				
Asp	Ser	Ala	Arg	Val	Pro	Tyr	Gly	Thr	Lys	Asp	Pro	Thr	Thr	Ile	Lys		
		35					40					45					
Gln	Phe	Gly	Leu	Glu	Ala	Leu	Asp	Phe	Phe	Lys	Pro	His	Gln	Ile	Lys		
	50					55					60						
Leu	Leu	Ile	Val	Ala	Cys	Asn	Thr	Ala	Ser	Ala	Leu	Ala	Leu	Glu	Glu		
65					70					75				80			
Met	Gln	Lys	His	Ser	Lys	Ile	Pro	Val	Val	Gly	Val	Ile	Glu	Pro	Ser		
			85						90					95			
Ile	Leu	Ala	Ile	Lys	Arg	Gln	Val	Lys	Asp	Lys	Asn	Ala	Pro	Ile	Leu		
		100						105					110				
Val	Leu	Gly	Thr	Lys	Ala	Thr	Ile	Gln	Ser	Asn	Ala	Tyr	Asp	Asn	Ala		
	115						120					125					
Leu	Lys	Gln	Gln	Gly	Tyr	Leu	Asn	Val	Ser	His	Leu	Ala	Thr	Ser	Leu		
	130					135					140						
Phe	Val	Pro	Leu	Ile	Glu	Glu	Ser	Ile	Leu	Glu	Gly	Glu	Leu	Leu	Glu		
145					150					155					160		
Thr	Cys	Met	Arg	Tyr	Tyr	Phe	Thr	Pro	Leu	Glu	Ile	Leu	Pro	Glu	Val		
			165						170					175			
Val	Ile	Leu	Gly	Cys	Thr	His	Phe	Pro	Leu	Ile	Ala	Gln	Lys	Ile	Glu		
		180						185					190				
Gly	Tyr	Phe	Met	Glu	His	Phe	Ala	Leu	Ser	Thr	Pro	Pro	Leu	Leu	Ile		
	195						200					205					
His	Ser	Gly	Asp	Ala	Ile	Val	Glu	Tyr	Leu	Gln	Gln	Asn	Tyr	Ala	Leu		
	210					215					220						
Lys	Lys	Asn	Ala	Cys	Ala	Phe	Pro	Lys	Val	Glu	Phe	His	Ala	Ser	Gly		
225					230					235					240		
Asp	Val	Val	Trp	Leu	Glu	Lys	Gln	Ala	Lys	Glu	Trp	Leu	Lys	Leu			
				245					250					255			

<210> 35  
 <211> 29

<212> DNA  
 <213> Homo sapiens

<400> 35  
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<210> 36  
 <211> 28  
 <212> DNA  
 <213> Homo sapiens

<400> 36  
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<210> 37  
 <211> 26  
 <212> DNA  
 <213> Homo sapiens

<400> 37  
 gcgaattcga tcagaatttt ttttct 26

<210> 38  
 <211> 26  
 <212> DNA  
 <213> Homo sapiens

<400> 38  
 ataagtactt gtgaatctta tactag 26

<210> 39  
 <211> 858  
 <212> DNA  
 <213> E. coli

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 cggcatctct taccggatct ccattacatt tatgctttcg ataacgtcgc tttcccgat 180  
 ggcgaaaaaa gcgaagcgtt tattgttgag cgagtgggtg caattgtcac cgcggtgcaa 240  
 gaacgttatc ccttgcgct ggctgtggtc gcttgcaaca ctgccagtac cgtttcactt 300  
 cctgcattac gcgaaaagtt cgacttcccg gttgttggtg tcgtgccggc gattaaacct 360  
 gctgcacgtc tgacggcaaa tggcattgtc ggattactgg caaccgcgg aacagttaaa 420  
 cgttcttata ctcatgagct gatcgcgcgt ttcgctaata aatgccagat agaaatgctg 480  
 ggctcggcag agatggttga gttggctgaa gcgaagctac atggcgaaga tgtttctctg 540  
 gatgcactaa aacgtatcct acgcccgtgg ttaagaatga aagagccgcc agataccggt 600  
 gtattgggtt gcacccattt cctctacta caagaagaac tgttacaagt gctgccagag 660  
 ggaacccggc tgggtggattc tggcgacgc attgctcgcc gaacggcctg gttgttagaa 720  
 catgaagccc cggatgcaaa atctgccgat gcgaatattg ccttttgtat ggcaatgacg 780  
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 ctggcagttt taggctga 858

<210> 40  
 <211> 285  
 <212> PRT  
 <213> E. coli

<400> 40

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			20					25					30		
Gly	Leu	Ser	Val	Tyr	Asp	Glu	Ile	Arg	His	Leu	Leu	Pro	Asp	Leu	His
			35				40					45			
Tyr	Ile	Tyr	Ala	Phe	Asp	Asn	Val	Ala	Phe	Pro	Tyr	Gly	Glu	Lys	Ser
	50					55					60				
Glu	Ala	Phe	Ile	Val	Glu	Arg	Val	Val	Ala	Ile	Val	Thr	Ala	Val	Gln
65					70				75						80
Glu	Arg	Tyr	Pro	Leu	Ala	Leu	Ala	Val	Val	Ala	Cys	Asn	Thr	Ala	Ser
				85				90						95	
Thr	Val	Ser	Leu	Pro	Ala	Leu	Arg	Glu	Lys	Phe	Asp	Phe	Pro	Val	Val
			100					105					110		
Gly	Val	Val	Pro	Ala	Ile	Lys	Pro	Ala	Ala	Arg	Leu	Thr	Ala	Asn	Gly
			115				120					125			
Ile	Val	Gly	Leu	Leu	Ala	Thr	Arg	Gly	Thr	Val	Lys	Arg	Ser	Tyr	Thr
	130					135					140				
His	Glu	Leu	Ile	Ala	Arg	Phe	Ala	Asn	Glu	Cys	Gln	Ile	Glu	Met	Leu
145					150				155						160
Gly	Ser	Ala	Glu	Met	Val	Glu	Leu	Ala	Glu	Ala	Lys	Leu	His	Gly	Glu
				165				170					175		
Asp	Val	Ser	Leu	Asp	Ala	Leu	Lys	Arg	Ile	Leu	Arg	Pro	Trp	Leu	Arg
			180					185					190		
Met	Lys	Glu	Pro	Pro	Asp	Thr	Val	Val	Leu	Gly	Cys	Thr	His	Phe	Pro
			195				200					205			
Leu	Leu	Gln	Glu	Glu	Leu	Leu	Gln	Val	Leu	Pro	Glu	Gly	Thr	Arg	Leu
	210					215					220				
Val	Asp	Ser	Gly	Ala	Ala	Ile	Ala	Arg	Arg	Thr	Ala	Trp	Leu	Leu	Glu
225					230					235					240
His	Glu	Ala	Pro	Asp	Ala	Lys	Ser	Ala	Asp	Ala	Asn	Ile	Ala	Phe	Cys
				245				250					255		
Met	Ala	Met	Thr	Pro	Gly	Ala	Glu	Gln	Leu	Leu	Pro	Val	Leu	Gln	Arg
			260					265					270		
Tyr	Gly	Phe	Glu	Thr	Leu	Glu	Lys	Leu	Ala	Val	Leu	Gly			
			275				280					285			

<210> 41  
 <211> 29  
 <212> DNA  
 <213> Homo sapiens

<400> 41  
 aaatagtcac atgaaaatag gcgttttttg

29

<210> 42  
 <211> 28  
 <212> DNA  
 <213> Homo sapiens

<400> 42  
 agaattctat tacaatttga gccattct

28

<210> 43  
 <211> 822  
 <212> DNA  
 <213> E. faecalis

&lt;400&gt; 43

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aaggaagcgc taaagcaatt accaaatgaa cgattaatth atttaggaga tacagcccgt 120
tgcccatatg gtccacgacc agccgaacaa gtcgttcagt ttacttggga aatggccgat 180
tttttattga aaaaacgaat aaaaatgcta gtaatcgcat gtaataccgc gacggctgtc 240
gcattagaag aaattaaagc tgccttgcca attccagttg ttggtgttat tttacctggc 300
gcacgagcag ccgttaaagt cacaaaaaat aacaaaattg gtgtcatagg taccttaggg 360
acaatcaaaa gtgcttccta tgaaatcgcc attaaaagta aggcaccagc aattgaggtg 420
actagtttag cttgccctaa atttgtcccc attggtgaaa gtaatcaata tcgttcttcc 480
gtagcaaaaa aaattgtggc agaaacactt caagcactac aattaaaagg acttgatacg 540
ttgatttttag gttgtaccca ttaccggttg ttacgtccgg tgattcaaaa tgtgatgggg 600
agtcatgtga cattaattga ctcaggagcc gaaacagttg gcgaagtcag catgcttctc 660
gattattttg acattgcccc cacgcctgaa gcgcctacac agcccatga atttataca 720
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&lt;210&gt; 44

&lt;211&gt; 273

&lt;212&gt; PRT

&lt;213&gt; E. faecalis

&lt;400&gt; 44

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 20          25          30
Ile Tyr Leu Gly Asp Thr Ala Arg Cys Pro Tyr Gly Pro Arg Pro Ala
 35          40          45
Glu Gln Val Val Gln Phe Thr Trp Glu Met Ala Asp Phe Leu Leu Lys
 50          55          60
Lys Arg Ile Lys Met Leu Val Ile Ala Cys Asn Thr Ala Thr Ala Val
 65          70          75          80
Ala Leu Glu Glu Ile Lys Ala Ala Leu Pro Ile Pro Val Val Gly Val
 85          90          95
Ile Leu Pro Gly Ala Arg Ala Ala Val Lys Val Thr Lys Asn Asn Lys
100          105          110
Ile Gly Val Ile Gly Thr Leu Gly Thr Ile Lys Ser Ala Ser Tyr Glu
115          120          125
Ile Ala Ile Lys Ser Lys Ala Pro Ala Ile Glu Val Thr Ser Leu Ala
130          135          140
Cys Pro Lys Phe Val Pro Ile Val Glu Ser Asn Gln Tyr Arg Ser Ser
145          150          155          160
Val Ala Lys Lys Ile Val Ala Glu Thr Leu Gln Ala Leu Gln Leu Lys
165          170          175
Gly Leu Asp Thr Leu Ile Leu Gly Cys Thr His Tyr Pro Leu Leu Arg
180          185          190
Pro Val Ile Gln Asn Val Met Gly Ser His Val Thr Leu Ile Asp Ser
195          200          205
Gly Ala Glu Thr Val Gly Glu Val Ser Met Leu Leu Asp Tyr Phe Asp
210          215          220
Ile Ala His Thr Pro Glu Ala Pro Thr Gln Pro His Glu Phe Tyr Thr
225          230          235          240
Thr Gly Ser Ala Lys Met Phe Glu Glu Ile Ala Ser Ser Trp Leu Gly
245          250          255
Ile Glu Asn Leu Lys Ala Gln Gln Ile His Leu Gly Gly Asn Glu Asn
260          265          270
Asp

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 <211> 801  
 <212> DNA  
 <213> S. aureus

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 tatgggccaa gaccaggaga acaagtaaaa caatatacag ttgaaatcgc tcgtaaatta 180  
 atggaatttg atataaaaat gctcgtgatt gcttgtaata ctgcaactgc tgtagcttta 240  
 gaatattttac aaaagacctt atcaatctca gtgattggcg taattgaacc aggtgctaga 300  
 acagcaataa tgacgactag aaatcaaaat gtattagtag taggaacgga aggcacaatt 360  
 aaatctgaag catatcgaac acatattaaa cgtataaatc cacatgtaga ggtacatggc 420  
 gttgcctgtc cagggtttgt gccacttgta gaacaaatga gatatagtga tccaacaatt 480  
 acaagcattg ttattcatca aacactgaaa cgttggcgta atagtgaagtc tgatactgtc 540  
 atttttaggat gtaccacta tccattgctc tataaaccta tctatgatta ttttggtggt 600  
 aaaaagacag tgatttcgtc tggattagaa acggctcgtg aagttagtgc attgctaaca 660  
 ttttagtaatg aacatgcaag ttatactgaa catccagatc atcgattttt tgcaacaggt 720  
 gataccacac atattactaa cattatcaaa gaatggctaa atttatctgt caatgtggaa 780  
 cgtatatcag tgaatgacta g 801

<210> 46  
 <211> 266  
 <212> PRT  
 <213> S. aureus

<400> 46  
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 Leu Gly Asp Ile Gly Arg Cys Pro Tyr Gly Pro Arg Pro Gly Glu Gln  
 35 40 45  
 Val Lys Gln Tyr Thr Val Glu Ile Ala Arg Lys Leu Met Glu Phe Asp  
 50 55 60  
 Ile Lys Met Leu Val Ile Ala Cys Asn Thr Ala Thr Ala Val Ala Leu  
 65 70 75 80  
 Glu Tyr Leu Gln Lys Thr Leu Ser Ile Ser Val Ile Gly Val Ile Glu  
 85 90 95  
 Pro Gly Ala Arg Thr Ala Ile Met Thr Thr Arg Asn Gln Asn Val Leu  
 100 105 110  
 Val Leu Gly Thr Glu Gly Thr Ile Lys Ser Glu Ala Tyr Arg Thr His  
 115 120 125  
 Ile Lys Arg Ile Asn Pro His Val Glu Val His Gly Val Ala Cys Pro  
 130 135 140  
 Gly Phe Val Pro Leu Val Glu Gln Met Arg Tyr Ser Asp Pro Thr Ile  
 145 150 155 160  
 Thr Ser Ile Val Ile His Gln Thr Leu Lys Arg Trp Arg Asn Ser Glu  
 165 170 175  
 Ser Asp Thr Val Ile Leu Gly Cys Thr His Tyr Pro Leu Leu Tyr Lys  
 180 185 190  
 Pro Ile Tyr Asp Tyr Phe Gly Gly Lys Lys Thr Val Ile Ser Ser Gly  
 195 200 205  
 Leu Glu Thr Ala Arg Glu Val Ser Ala Leu Leu Thr Phe Ser Asn Glu  
 210 215 220  
 His Ala Ser Tyr Thr Glu His Pro Asp His Arg Phe Phe Ala Thr Gly  
 225 230 235 240  
 Asp Thr Thr His Ile Thr Asn Ile Ile Lys Glu Trp Leu Asn Leu Ser  
 245 250 255

Val Asn Val Glu Arg Ile Ser Val Asn Asp  
260 265

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<211> 822  
<212> DNA  
<213> E. faecium

<400> 47  
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actgtagtaa aagaagccct gaaacaatta ccgaatgaaa atattttatt tgtaggagac 120  
acagcacgct gcccatatgg ccctagaccc gcggaacagg taatccagta tacttgggaa 180  
atgacggatt atctgggtgga gcaaggaatc aagatgctgg tgatcgctg caataccgca 240  
actgcgggtg ctttagaaga aatcaaagct gctctttcta ttccagtcac cgggtgtgatc 300  
cttcccggtg ctagagcggc agtaaaaaaa acacaaaata aacaagttgg cattatcggc 360  
acgattggta cggtaaaaaa tcaagcttat gaaaaagcac tgaaagagaa agtaccagaa 420  
ttgactgtga caagtcttgc ttgtccaaaa tttgtttcag ttgtcgaaag taatgaatac 480  
cattcatcgg tggcgaaaaa aattgtggca gaaacattag ctcctttaac cactaaaaaa 540  
atcgatacat tgattttggg atgcacccat tatccattat tacgccccat cattcaaaat 600  
gtaatgggag aaaatgttca actgatcgat tctggagcag aaacagtagg tgaagtatct 660  
atgctgttag attatttcaa tctgagcaat tcaccgcaaa atggtcggac attatgccag 720  
ttttatacaa ctggctctgc caaacttttc gaggaatatg ctgaagactg gcttggaatc 780  
ggacacttaa atgtagaaca tatcgaattg ggaggaaaat aa 822

<210> 48  
<211> 273  
<212> PRT  
<213> E. faecium

<400> 48  
Met Ile Arg Leu Thr Asp Asn Arg Pro Ile Gly Phe Ile Asp Ser Gly  
1 5 10 15  
Val Gly Gly Leu Thr Val Val Lys Glu Ala Leu Lys Gln Leu Pro Asn  
20 25 30  
Glu Asn Ile Leu Phe Val Gly Asp Thr Ala Arg Cys Pro Tyr Gly Pro  
35 40 45  
Arg Pro Ala Glu Gln Val Ile Gln Tyr Thr Trp Glu Met Thr Asp Tyr  
50 55 60  
Leu Val Glu Gln Gly Ile Lys Met Leu Val Ile Ala Cys Asn Thr Ala  
65 70 75 80  
Thr Ala Val Ala Leu Glu Glu Ile Lys Ala Ala Leu Ser Ile Pro Val  
85 90 95  
Ile Gly Val Ile Leu Pro Gly Thr Arg Ala Ala Val Lys Lys Thr Gln  
100 105 110  
Asn Lys Gln Val Gly Ile Ile Gly Thr Ile Gly Thr Val Lys Ser Gln  
115 120 125  
Ala Tyr Glu Lys Ala Leu Lys Glu Lys Val Pro Glu Leu Thr Val Thr  
130 135 140  
Ser Leu Ala Cys Pro Lys Phe Val Ser Val Val Glu Ser Asn Glu Tyr  
145 150 155 160  
His Ser Ser Val Ala Lys Lys Ile Val Ala Glu Thr Leu Ala Pro Leu  
165 170 175  
Thr Thr Lys Lys Ile Asp Thr Leu Ile Leu Gly Cys Thr His Tyr Pro  
180 185 190  
Leu Leu Arg Pro Ile Ile Gln Asn Val Met Gly Glu Asn Val Gln Leu  
195 200 205  
Ile Asp Ser Gly Ala Glu Thr Val Gly Glu Val Ser Met Leu Leu Asp  
210 215 220

Tyr Phe Asn Leu Ser Asn Ser Pro Gln Asn Gly Arg Thr Leu Cys Gln  
 225 230 235 240  
 Phe Tyr Thr Thr Gly Ser Ala Lys Leu Phe Glu Glu Ile Ala Glu Asp  
 245 250 255  
 Trp Leu Gly Ile Gly His Leu Asn Val Glu His Ile Glu Leu Gly Gly  
 260 265 270  
 Lys

<210> 49  
 <211> 335  
 <212> DNA  
 <213> E. saccharolyticus

<400> 49  
 gcatgtaata ccgcaacggc ggtagcggtta gaagaaatta aagcgcaatt agatattcca 60  
 gtcgctcggtg tgatcttacc tggtagctgt gctgcagtta aagctacgaa aaatcgtcaa 120  
 atcgggtatta taggaacagc gggtagcaatt aaaagtagtt cgtatgagca agcaattaaa 180  
 atgaaagtgc ctgaagcatc ggtgactagt ttagcttgct ctaaatttgt accgattggt 240  
 gaaagtaatc aatttcaatc atcggtagct aaaaaaattg ttgctgagac gttattacca 300  
 ttgcaacata aaaaattaga tacgttgatt ttagg 335

<210> 50  
 <211> 111  
 <212> PRT  
 <213> E. saccharolyticus

<400> 50  
 Ala Cys Asn Thr Ala Thr Ala Val Ala Leu Glu Glu Ile Lys Ala Gln  
 1 5 10 15  
 Leu Asp Ile Pro Val Val Gly Val Ile Leu Pro Gly Thr Arg Ala Ala  
 20 25 30  
 Val Lys Ala Thr Lys Asn Arg Gln Ile Gly Ile Ile Gly Thr Ala Gly  
 35 40 45  
 Thr Ile Lys Ser Ser Ser Tyr Glu Gln Ala Ile Lys Met Lys Val Pro  
 50 55 60  
 Glu Ala Ser Val Thr Ser Leu Ala Cys Pro Lys Phe Val Pro Ile Val  
 65 70 75 80  
 Glu Ser Asn Gln Phe Gln Ser Ser Val Ala Lys Lys Ile Val Ala Glu  
 85 90 95  
 Thr Leu Leu Pro Leu Gln His Lys Lys Leu Asp Thr Leu Ile Leu  
 100 105 110

<210> 51  
 <211> 344  
 <212> DNA  
 <213> E mundtii

<400> 51  
 gtaatcgcat gtaataccgc aactgcggtc gcattagaag aaatcaaagc aacactctcg 60  
 attccagtga tcggtgtgat tttgccagga acgagagcgg cagtcaagca gacgaaaaat 120  
 catcgagtag ggggtgattgg aacaattggg accgtcaaaa gtgctgctta cgagacggca 180  
 ttattggata aagcaccgga actgaaagt accagcttgg cgtgtccaaa gtttgtttca 240  
 gtcgtagaaa gtaaagaata ccgatcatca gtcgctaaaa aaatcgtggc tcaaactttg 300  
 cttccattag aattaaagg gatcgatagc ttgattttag gttg 344

<210> 52



<211> 113  
 <212> PRT  
 <213> E. mundtii

<400> 52  
 Val Ile Ala Cys Asn Thr Ala Thr Ala Val Ala Leu Glu Glu Ile Lys  
 1 5 10 15  
 Ala Thr Leu Ser Ile Pro Val Ile Gly Val Ile Leu Pro Gly Thr Arg  
 20 25 30  
 Ala Ala Val Lys Gln Thr Lys Asn His Arg Val Gly Val Ile Gly Thr  
 35 40 45  
 Ile Gly Thr Val Lys Ser Ala Ala Tyr Glu Thr Ala Leu Leu Asp Lys  
 50 55 60  
 Ala Pro Glu Leu Lys Val Thr Ser Leu Ala Cys Pro Lys Phe Val Ser  
 65 70 75 80  
 Val Val Glu Ser Lys Glu Tyr Arg Ser Ser Val Ala Lys Lys Ile Val  
 85 90 95  
 Ala Gln Thr Leu Leu Pro Leu Glu Leu Lys Gly Ile Asp Thr Leu Ile  
 100 105 110  
 Leu

<210> 53  
 <211> 340  
 <212> DNA  
 <213> E. casseliflavus

<400> 53  
 atcgcatgta ataccgcgac agcgggtcgcc cttgaagaaa tcaaagaaca actaacgatac 60  
 ccagtgatcg gcgtgatcct gcctggcagt cgagcagcag tcaaagcaag caaaaaccaa 120  
 cgaatcggtg tcatcgggac aaacggaacg atcaaaagtg actcttataa gcgcgcgctt 180  
 catggcaaaag cgccccatgc gtccgctcgtc agtttggtt gcccgaaagt tgtgccgatac 240  
 gtagaaagca aacaatacca tagctcggtc gccaaagaaa tcgtggcaga aacgttgcgt 300  
 ccattgaaaa acaaacggct agatacgttg attttaggtg 340

<210> 54  
 <211> 112  
 <212> PRT  
 <213> E. casseliflavus

<400> 54  
 Ile Ala Cys Asn Thr Ala Thr Ala Val Ala Leu Glu Glu Ile Lys Glu  
 1 5 10 15  
 Gln Leu Thr Ile Pro Val Ile Gly Val Ile Leu Pro Gly Ser Arg Ala  
 20 25 30  
 Ala Val Lys Ala Ser Lys Asn Gln Arg Ile Gly Val Ile Gly Thr Asn  
 35 40 45  
 Gly Thr Ile Lys Ser Asp Ser Tyr Lys Arg Ala Leu His Gly Lys Ala  
 50 55 60  
 Pro His Ala Ser Val Val Ser Leu Ala Cys Pro Lys Phe Val Pro Ile  
 65 70 75 80  
 Val Glu Ser Lys Gln Tyr His Ser Ser Val Ala Lys Lys Ile Val Ala  
 85 90 95  
 Glu Thr Leu Arg Pro Leu Lys Asn Lys Arg Leu Asp Thr Leu Ile Leu  
 100 105 110

<210> 55

<211> 337  
 <212> DNA  
 <213> *E. flavescens*

<400> 55  
 atcgcatgta ataccgcgac agcgggtcgcc cttgaagaaa tcaaagaaca actaacgatac 60  
 ccagtgatcg gcgtgatacct gcctggcagt cgagcagcag tcaaagcaag caaaaaccaa 120  
 cgaatcggtg tcatcgggac aaacggaacg atcaaaagtg actcttataa gcgcgcgctt 180  
 catggcaaag cgcccatgc gtccgtcgtc agtttggtt gccgaagt tgtgccgatac 240  
 gtagaaagca aacaatacca tagctcggtc gccaaagaaa tcgtggcaga aacgttgcgt 300  
 ccattgaaaa acaaacggct agatacgtt attttag 337

<210> 56  
 <211> 112  
 <212> PRT  
 <213> *E. flavescens*

<400> 56  
 Ile Ala Cys Asn Thr Ala Thr Ala Val Ala Leu Glu Glu Ile Lys Glu  
 1 5 10 15  
 Gln Leu Thr Ile Pro Val Ile Gly Val Ile Leu Pro Gly Ser Arg Ala  
 20 25 30  
 Ala Val Lys Ala Ser Lys Asn Gln Arg Ile Gly Val Ile Gly Thr Asn  
 35 40 45  
 Gly Thr Ile Lys Ser Asp Ser Tyr Lys Arg Ala Leu His Gly Lys Ala  
 50 55 60  
 Pro His Ala Ser Val Val Ser Leu Ala Cys Pro Lys Phe Val Pro Ile  
 65 70 75 80  
 Val Glu Ser Lys Gln Tyr His Ser Ser Val Ala Lys Lys Ile Val Ala  
 85 90 95  
 Glu Thr Leu Arg Pro Leu Lys Asn Lys Arg Leu Asp Thr Leu Ile Leu  
 100 105 110

<210> 57  
 <211> 341  
 <212> DNA  
 <213> *E. cecorum*

<400> 57  
 atcgcatgta ataccgcgac tgcagcagct ttaacccaaa ttaaggaaca attagacatt 60  
 ccagttgtcg gtgtgatttt acctggaact agagctgctg tcaaaaatac aaaatcgcaa 120  
 cgaattggga ttatcggcac acaaggaacc atccaaagtg gcagttatga acaagccatt 180  
 ctttctaaag taccgactgc tcaacctgtg agtttagcgt gtcctagatt tgttccgata 240  
 gtagaaagta atcaagcaaa ttcaagtgtg gcaaaaaaaa ttgtcgctca aacactataa 300  
 ccgatgacga aaaaaaacat cgatacgtt attttaggtt g 341

<210> 58  
 <211> 112  
 <212> PRT  
 <213> *E. cecorum*

<400> 58  
 Ile Ala Cys Asn Thr Ala Thr Ala Ala Leu Thr Gln Ile Lys Glu  
 1 5 10 15  
 Gln Leu Asp Ile Pro Val Val Gly Val Ile Leu Pro Gly Thr Arg Ala  
 20 25 30  
 Ala Val Lys Asn Thr Lys Ser Gln Arg Ile Gly Ile Ile Gly Thr Gln  
 35 40 45

Gly	Thr	Ile	Gln	Ser	Gly	Ser	Tyr	Glu	Gln	Ala	Ile	Leu	Ser	Lys	Val
50					55					60					
Pro	Thr	Ala	Gln	Pro	Val	Ser	Leu	Ala	Cys	Pro	Arg	Phe	Val	Pro	Ile
65				70					75					80	
Val	Glu	Ser	Asn	Gln	Ala	Asn	Ser	Ser	Val	Ala	Lys	Lys	Ile	Val	Ala
			85					90					95		
Gln	Thr	Leu	Gln	Pro	Met	Thr	Lys	Lys	Asn	Ile	Asp	Thr	Leu	Ile	Leu
		100						105					110		

<210> 59  
 <211> 339  
 <212> DNA  
 <213> E. raffinosus

<400> 59  
 atcgcatgta ataccgcgac ggcagtagct ttggaagaaa ttaaaagaac cgtagatatt 60  
 cccgtaatcg gtgttatata gccaggatct cgcgcagcgt taaaggcaag cgaaaatggg 120  
 cgcgtgggaa ttatcggaac cattggaaca gtaaaaagtg gttcttataa acacgaacta 180  
 caggaaaaag ctcttgatac ttatgtttct agtttagcat gcccaaaatt tgtaccgatt 240  
 gttgaaagta atcaatttaa tagctcggtg gcgaaaaaaa ttgtttctca aacattaact 300  
 cctttgaaaa aggaaaagtt ggatacgttg attttaggt 339

<210> 60  
 <211> 112  
 <212> PRT  
 <213> E. raffinosus

Ile	Ala	Cys	Asn	Thr	Ala	Thr	Ala	Val	Ala	Leu	Glu	Glu	Ile	Lys	Arg
1			5					10					15		
Thr	Val	Asp	Ile	Pro	Val	Ile	Gly	Val	Ile	Gln	Pro	Gly	Ser	Arg	Ala
		20				25					30				
Ala	Leu	Lys	Ala	Ser	Glu	Asn	Gly	Arg	Val	Gly	Ile	Ile	Gly	Thr	Ile
	35					40				45					
Gly	Thr	Val	Lys	Ser	Gly	Ser	Tyr	Lys	His	Glu	Leu	Gln	Glu	Lys	Ala
50				55				60							
Pro	Asp	Thr	Tyr	Val	Ser	Ser	Leu	Ala	Cys	Pro	Lys	Phe	Val	Pro	Ile
65				70				75						80	
Val	Glu	Ser	Asn	Gln	Phe	Asn	Ser	Ser	Val	Ala	Lys	Lys	Ile	Val	Ser
			85					90					95		
Gln	Thr	Leu	Thr	Pro	Leu	Lys	Lys	Glu	Lys	Leu	Asp	Thr	Leu	Ile	Leu
		100						105					110		

<210> 61  
 <211> 341  
 <212> DNA  
 <213> E. malodoratus

<400> 61  
 atcgcatgta ataccgcaac cgcagtggct ttagaagaga ttaagaagaa cgttgatatt 60  
 cctgttattg gtgttatcca accaggatca cgtgctgcat taaaagcaag taaaaatagt 120  
 cgtgtaggta tcatcggaac actaggaact gtaaaaagtg gatcttataa acatgagctg 180  
 caagaaaaag caccagaaac gtatgttgct agtctggcct gcccaaaatt tgtgccaatc 240  
 gttgaaagta atcagtttaa tagttctgta gccaaaaaga ttgtttcaca atctctggca 300  
 cccttaaaaa aggaaaaatt agatacgttg attttaggtt g 341

<210> 62

<211> 112  
 <212> PRT  
 <213> E. malodoratus

<400> 62  
 Ile Ala Cys Asn Thr Ala Thr Ala Val Ala Leu Glu Glu Ile Lys Lys  
 1 5 10 15  
 Asn Val Asp Ile Pro Val Ile Gly Val Ile Gln Pro Gly Ser Arg Ala  
 20 25 30  
 Ala Leu Lys Ala Ser Lys Asn Ser Arg Val Gly Ile Ile Gly Thr Leu  
 35 40 45  
 Gly Thr Val Lys Ser Gly Ser Tyr Lys His Glu Leu Gln Glu Lys Ala  
 50 55 60  
 Pro Glu Thr Tyr Val Ala Ser Leu Ala Cys Pro Lys Phe Val Pro Ile  
 65 70 75 80  
 Val Glu Ser Asn Gln Phe Asn Ser Ser Val Ala Lys Lys Ile Val Ser  
 85 90 95  
 Gln Ser Leu Ala Pro Leu Lys Lys Glu Lys Leu Asp Thr Leu Ile Leu  
 100 105 110

<210> 63  
 <211> 338  
 <212> DNA  
 <213> E. solitarus

<400> 63  
 gcatgtaata ccgcaacagc tgtggcttta gatgagatta aagagcaact gcaaateccct 60  
 gttgtgggag ttattatgcc gggaaccaga gcagctgtta aagcgactaa aaatcatcgt 120  
 attggtgtga ttggcacaaa aggaacagtt aaaagtgcct cttacaaacg agcaatcaaa 180  
 gaaaaaatg aaaatacaaaa agtaacaagt ttggcttgct cgaagtttgt tccattgtg 240  
 gaaagtaatc aaattcattc ttcagtggca aaaaaaattg tatttgaaac actattaccc 300  
 ttaaaaaata aacatttaga tacgttgatt ttaggttg 338

<210> 64  
 <211> 111  
 <212> PRT  
 <213> E. solitarus

<400> 64  
 Ala Cys Asn Thr Ala Thr Ala Val Ala Leu Asp Glu Ile Lys Glu Gln  
 1 5 10 15  
 Leu Gln Ile Pro Val Val Gly Val Ile Met Pro Gly Thr Arg Ala Ala  
 20 25 30  
 Val Lys Ala Thr Lys Asn His Arg Ile Gly Val Ile Gly Thr Lys Gly  
 35 40 45  
 Thr Val Lys Ser Ala Ser Tyr Lys Arg Ala Ile Lys Glu Lys Asn Glu  
 50 55 60  
 Asn Thr Lys Val Thr Ser Leu Ala Cys Pro Lys Phe Val Pro Ile Val  
 65 70 75 80  
 Glu Ser Asn Gln Ile His Ser Ser Val Ala Lys Lys Ile Val Phe Glu  
 85 90 95  
 Thr Leu Leu Pro Leu Lys Asn Lys His Leu Asp Thr Leu Ile Leu  
 100 105 110

<210> 65  
 <211> 341  
 <212> DNA

<213> E. hirae

<400> 65  
 atcgcatgta ataccgctac tgcggttgct ttagaagaaa tcaaggcggc acttcctatt 60  
 ccagtcattg gtgtgatctt acctgggaca agagcagctg ttaaacaac aagaaataaa 120  
 caagtaggga ttatcggaac cctcggaacg atcaaaagtc gtgcttatga aacagcgctg 180  
 aaaacgaagg tacctgaact tgcggtgact agtttggtt gtccaaaatt cgtttcggta 240  
 gtggaaagta atgaatatca ttcgtcagtg gcaaaaaaaa tcgttgccca gacactagcg 300  
 ccattgggta ctaagaaaat cgatacgttg attttagggt g 341

<210> 66  
 <211> 111  
 <212> PRT  
 <213> E. hirae

<400> 66  
 Ala Cys Asn Thr Ala Thr Ala Val Ala Leu Glu Glu Ile Lys Ala Ala  
 1 5 10 15  
 Leu Pro Ile Pro Val Ile Gly Val Ile Leu Pro Gly Thr Arg Ala Ala  
 20 25 30  
 Val Lys Gln Thr Arg Asn Lys Gln Val Gly Ile Ile Gly Thr Leu Gly  
 35 40 45  
 Thr Ile Lys Ser Arg Ala Tyr Glu Thr Ala Leu Lys Thr Lys Val Pro  
 50 55 60  
 Glu Leu Ala Val Thr Ser Leu Ala Cys Pro Lys Phe Val Ser Val Val  
 65 70 75 80  
 Glu Ser Asn Glu Tyr His Ser Ser Val Ala Lys Lys Ile Val Ala Gln  
 85 90 95  
 Thr Leu Ala Pro Leu Val Thr Lys Lys Ile Asp Thr Leu Ile Leu  
 100 105 110

<210> 67  
 <211> 29  
 <212> DNA  
 <213> Homo sapiens

<400> 67  
 aaatagtcac atgaaaatag gcgttttttg 29

<210> 68  
 <211> 28  
 <212> DNA  
 <213> Homo sapiens

<400> 68  
 agaattctat tacaatttga gccattct 28

<210> 69  
 <211> 26  
 <212> DNA  
 <213> Homo sapiens

<400> 69  
 gcgaattcga tcagaatttt ttttct 26

<210> 70  
 <211> 26  
 <212> DNA

<213> Homo sapiens

<400> 70  
ataagtactt gtgaatctta tactag 26

<210> 71  
<211> 29  
<212> DNA  
<213> Homo sapiens

<400> 71  
aaaatgctag taatcgcgatg taataccgc 29

<210> 72  
<211> 26  
<212> DNA  
<213> Homo sapiens

<400> 72  
tgggtacaac ctaaaatcaa cgtatc 26

<210> 73  
<211> 765  
<212> DNA  
<213> Aquifex pyrophilus NA sequence

<400> 73  
atgaagatag gtatctttga cagtgggtgtg gggggactta ctgttctaaa ggctataaga 60  
aatagatata gaaagggttg tatagtatac ctcggtgata ccgcaagggt tccctacggc 120  
ataagggtcta aagatacgat aatcagatac tcccttgagt gtgcgggctt tttaaaggat 180  
aagggtgttg atataatcgt cgttgccctgc aataccgcaa gtgcttacgc tcttgaacgt 240  
ttaaagaaaag agataaacgt tcccgttttc ggcgttattg aaccgggggt taaagaagcc 300  
ttaaaaaagt caaggaataa aaaaatagga gttataggaa ctccctgcaac cgtaaaaagc 360  
ggagcctacc agagaaagct tgaagagggg ggagctgatg tttttgcaaa ggcctgtccc 420  
ctattcgttc cccttgcgga ggaagggtctc cttgaggggg agataacaag aaagggttgta 480  
gaacactacc ttaaggagtt taaaggtaag attgatactc tgattttagg atgtacccat 540  
taccctcttc ttaaaaagga gataaagaag tttttgggag acgttgaagt cgttgactct 600  
tccgaagccc tttcccttcc cctccataac tttataaagg acgatgggtc ctcatccctt 660  
gagttatttt ttacggacct ttccccaaat ctccagtttt tgattaaatt aatactcggg 720  
agggattacc cggtaaaact tgcggagggg gtttttacac attaa 765

<210> 74  
<211> 262  
<212> PRT  
<213> Aquifex pyrophilus amino acid sequence

<400> 74  
Met Lys Ile Gly Ile Phe Asp Ser Gly Val Gly Gly Leu Thr Val Leu  
1 5 10 15  
Lys Ala Ile Arg Asn Arg Tyr Arg Lys Val Asp Ile Val Tyr Leu Gly  
20 25 30  
Asp Thr Ala Arg Val Pro Tyr Gly Ile Arg Ser Lys Asp Phe Thr Thr  
35 40 45  
Ile Ile Arg Tyr Ser Leu Glu Cys Ala Gly Phe Leu Lys Asp Lys Gly  
50 55 60  
Val Asp Ile Ile Val Val Ala Cys Asn Thr Ala Ser Ala Tyr Ala Leu  
65 70 75 80  
Glu Arg Leu Lys Lys Glu Ile Asn Val Pro Val Phe Gly Val Ile Glu  
85 90 95

Pro Gly Val Lys Glu Ala Leu Lys Lys Ser Phe Thr Arg Asn Lys Lys  
 100 105 110  
 Ile Gly Val Ile Gly Thr Pro Ala Thr Val Lys Ser Gly Ala Tyr Gln  
 115 120 125  
 Arg Lys Leu Glu Glu Gly Gly Ala Asp Val Phe Ala Lys Ala Cys Pro  
 130 135 140  
 Leu Phe Val Pro Leu Ala Glu Glu Gly Leu Leu Glu Gly Glu Ile Thr  
 145 150 155 160  
 Arg Lys Val Val Glu His Tyr Phe Thr Leu Lys Glu Phe Lys Gly Lys  
 165 170 175  
 Ile Asp Thr Leu Ile Leu Gly Cys Thr His Tyr Pro Leu Leu Lys Lys  
 180 185 190  
 Glu Ile Lys Lys Phe Leu Gly Asp Val Glu Val Val Asp Ser Ser Glu  
 195 200 205  
 Ala Leu Ser Leu Ser Leu His Asn Phe Ile Lys Asp Asp Gly Ser Ser  
 210 215 220  
 Ser Leu Glu Leu Phe Thr Phe Phe Thr Asp Leu Ser Pro Asn Leu Gln  
 225 230 235 240  
 Phe Leu Ile Lys Leu Ile Leu Gly Arg Asp Tyr Pro Val Lys Leu Ala  
 245 250 255  
 Glu Gly Val Phe Thr His  
 260

<210> 75  
 <211> 19  
 <212> DNA  
 <213> Homo sapiens

<400> 75  
 tgatgcaaca aatggacga

19

<210> 76  
 <211> 18  
 <212> DNA  
 <213> Homo sapiens

<400> 76  
 ttacaatttg agccattc

18